

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 22:55:45 ; Search time 3287 Seconds

(without alignments)
9615:138 Million cell updates/sec

Title: US-10-686-428A-3_COPY_444_999

Perfect score: 556

Sequence: 1 aaggagcatgggcccgg.....catcagccagtgaaaggga 556

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	3000	4 SSPAI1	Y11347 S.scrofa mr
2	480.8	86.5	2970	4 BTPAI1MR	X16383 Bovine mRNA
3	461.2	82.9	844	4 AF508034	Equus cab
4	455.2	81.9	1209	11 AY888695	Synthetic
5	455.2	81.9	1209	11 AY889067	AY889067 Synthetic
6	455.2	81.9	1209	11 AY891356	AY891356 Synthetic
7	455.2	81.9	1209	11 AY891655	AY891655 Synthetic
8	455.2	81.9	1209	11 AY893400	AY893400 Synthetic
9	455.2	81.9	1209	11 AY893851	AY893851 Synthetic
10	455.2	81.9	1532	6 CQ716284	CQ716284 Sequence
11	455.2	81.9	1962	8 HSPAI1	X04744 Human mRNA
12	455.2	81.9	2207	8 BC010860	BC010860 Homo sapi
13	455.2	81.9	2660	6 CQ413075	CQ413075 Sequence
14	455.2	81.9	2876	6 AR106060	AR106060 Sequence
15	455.2	81.9	2876	6 AR106066	AR106066 Sequence
16	455.2	81.9	2876	6 BD094083	BD094083 Shear str
17	455.2	81.9	2876	6 CQ776713	CQ776713 Sequence
18	455.2	81.9	2876	6 AR258505	AR258505 Sequence

C	19	455.2	81.9	2876	6	AR258511	Sequence
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	23	455.2	81.9	2937	6	CQ861596	Sequence
	24	455.2	81.9	2937	8	HUMPAIB	Human beta-
	25	455.2	81.9	2944	6	I08667	Sequence 4
	26	455.2	81.9	3171	6	AX281751	Sequence
	27	453.6	81.6	1209	11	AY891093	AY891093 Synthetic
	28	453.6	81.6	1482	6	AX787059	AX787059 Sequence
	29	453.6	81.6	1482	8	HSPAIR	X04429 Human mRNA
	30	452	81.3	2970	4	MVPAI1	X58541 Mink mRNA f
	31	447.2	80.4	1187	6	CQ785751	Sequence
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	33	447.2	80.4	1209	8	AF393201	AF393201 Cercopith
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	35	426.8	76.8	548	4	AF074325	AF074325 Oryctolag
	36	420	75.5	3053	6	AX827499	AX827499 Sequence
	37	420	75.5	3053	9	RATPAI1A	M24067 Rattus norv
	38	415.2	74.7	2741	9	BC054091	BC054091 Mus muscu
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	41	294.4	52.9	1155	6	BD091054	BD091054 DNA chip
	42	286.2	51.5	9360	8	HSM809316	EX649164 Homo sapi
	43	218.6	39.3	249	4	BTPAI1	X52906 Bovine PAI-
	44	213.4	38.4	263	4	AF069712	AF069712 Oryctolag
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ALIGNMENTS

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LOCUS	S.scrofa mRNA for plasminogen activator inhibitor-1.				
DEFINITION	Y11347.1				
ACCESSION	Y11347.1				
VERSION	GI:1870169				
KEYWORDS	PAI-1 protein; PLANH1 gene; plasminogen activator inhibitor-1.				
SOURCE	Sus scrofa (pig)				
ORGANISM	Sus scrofa				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.				
REFERENCE	1				
AUTHORS	Bijmens, A.P., Knockaert, I., Cousin, E., Kruihof, E.K. and Declerck, P.J.				
TITLE	Expression and characterization of recombinant porcine plasminogen activator inhibitor-1				
JOURNAL	Thromb. Haemost. 77 (2), 350-356 (1997)				
PUBMED	9157595				
REFERENCE	2	(bases 1 to 3000)			
AUTHORS	Kruihof, E.K.O.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-FEB-1997) E.K.O. Kruihof, Division of Angiology and Hemostasis, University Hospital Geneva, CH-1211 Geneva, SWITZERLAND				
FEATURES	Location/Qualifiers				
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QY 61 CAGCGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGACC 120
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Db 504 CAGCGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGACC 563
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QY 121 ACGGTCACGACGTGATTTTCAGAGATGGACAGCCAGGTCATCATCAATGACTGG 180
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Db 564 ACGGTCACGACGTGATTTTCAGAGATGGACAGCCAGGTCATCATCAATGACTGG 623
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QY 181 GTGAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCAG 240
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|
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QY 241 CTGACGGCGCTGGTCTGTGTAATGCGCTCTACTTCAACGGCCAGTGGAAACGCCCTTC 300
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QY 301 CCAGAGAAAGCACTCACACCGCTCTCCACAGTCTGTAGTGGCAGCACCGTCTCTGTG 360
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Db 744 CCAGAGAAAGCACTCACACCGCTCTCCACAGTCTGTAGTGGCAGCACCGTCTCTGTG 803
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Db 804 CCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCCCGCAGGCCAT 863
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Db 984 AGCCAGTGGAAAGGGA 999
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|
|

RESULT 2
BTPIILMR 2970 bp mRNA linear MAM 18-APR-2005
LOCUS Bovine mRNA for Plasminogen activator inhibitor (PAI-1).
DEFINITION X16383
ACCESSION PAI-1 gene; plasminogen activator inhibitor
VERSION inhibitor type 1.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2970)
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AUTHORS Mimuro,J., Sawdey,M., Hattori,M. and Luskutoff,D.J.
TITLE cDNA for bovine type 1 plasminogen activator inhibitor (PAI-1)
JOURNAL Nucleic Acids Res. 17 (21), 8872 (1989)
PUBMED 2587231
REFERENCE 2 (bases 1 to 2970)
AUTHORS Sawdey,M.S.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-1989) Sawdey M.S., Research Institute of Scripps
Clinic, 10666 No Torrey Pines Road, La Jolla CA 92014, U S A
FEATURES
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1..2970
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/cell_line="aortic endothelial"
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1442..1453
misc_feature
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Best Local Similarity 91.5%; Pred. No. 1.5e-102;
Matches 509; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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|
Db 428 AAGGAGCTCATGGGCGGTGGGAACAAAGATGAGATCAGCACGGCGATGCCATCTTCGTG 487
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QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 120
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Db 488 CAGCGGACCTAGAGCTGGTCCATGGTTTCATGCCCACTTCTTCAGGCTGTTCGGTACC 547
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QY 121 ACGGTCACGAGGTGGATTTTTCAGAGATGACAGACGACGAGTTCATCAATGACTGG 180
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Db 548 ACGGTCACGAGGTGACTTCTCTGAAGTGAGAGAGCCAGGTTTCATCCTCAACGACTGG 607
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QY 181 GTGAAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAGGGGCTGTGGACCAG 240
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QY 241 CTGACGGCGCTGGTCTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAACGCCCTTC 300
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Db 668 CTGACACGCCCTGGTCTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGTGCCTTC 727
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|
|
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCACAAGTCTGTAGTGGCAGCACCGTCTCTGTG 360
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Db 728 CCAGAGTCAAAACACCCACCGCTCTTCCACAAGTCCGATGGCAGCACCATCTCTGTG 787
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QY 361 CCCATGATGGCTCAGACCAACAAAGTTCACACTGAGTTTTCACCCCGCAGCGCCAT 420
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Db 788 CCCATGATGGCTCAGACCAACAAAGTTCACACTGAGTTTTCACCCCGCAGCGCCGT 847
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QY 421 TACTACGACATCTCGGAATTGCCCTTACCACGGCAACACTCTGAGCATGTTTCATTCGCCGC 480
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181  ACACAAAGGCATGATCAGCGACTTACTTTCAGCAAGGGCGGTGACGAGCTGACGCC 240
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241  TGGTGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCCCTTCCAGAGTCGG 300
311  GCATCTACCAACCGCTCTTCCCAAGTCTGATGGCAGCACCGTCTCTGTGCCCCATGAG 370
301  GCACCCACCAACCGCTCTTCCCAAGTCTGATGGCAGCACCGCTCTGTGTCCATGATGG 360
371  CTCAGACCAACAAGTTCAACTACACTCAGTGTTCCTCCACCCCGCAGCGGCATTACTACGACA 430
361  CTCAGACCAACAAGTTCAACTATGCTGAGTTTACCACCCCTGACGGCCATTACTACGACA 420
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421  TCTCTGAATTCGCCCTTACCAACGGGACACCCCTCAGCATGTTCAATTCGCCGCTCCCTATGAAA 480
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481  AAGAGTGTGCTCTCTCTGCCCTCACCACCAATTCTGGATGCCGCTCATCAGCCAGTGA 540
551  AAGGGA 556
541  AAGGA 546

RESULT 4
AY888695
LOCUS
DEFINITION
AY888695
1209 bp mRNA linear SYN 22-MAR-2005
Synthetic construct Homo sapiens clone FLH031026.01X serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
complete cds.
ACCESSION
AY888695
VERSION
AY888695.1 GI:61358892
KEYWORDS
Human ORF Project.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 1209)
AUTHORS
Shen,B., Rolfs,A., Jenson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Cloning of human full-length CDS in Creator (TM) recombinational
vector system
Unpublished
JOURNAL
2 (bases 1 to 1209)
REFERENCE
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Direct Submission
TITLE
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
COMMENT
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using BD In-Fusion(TM) cloning system
between the SalI and HindIII sites of the pBMR-Dual vector.
Additional sequences in the clone: 'ACC' after SalI site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
clonally isolated and full-length sequence-verified.
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1..1209
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1..1209
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ORIGIN
Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
1 AAGGAGCTCATGGGCGCGTGGAAACAAGATGATCAGCACGCGCGATGCCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGCGCGTGGAAACAAGATGATCAGCACGCGCGATCTTCGTC 366
Qy 61 CAGCGGATCTGAAGCTGCTCAGGCTTTCATGCCCTACTTCTTCAGGCTGTCGGACC 120
Db 367 CAGCGGATCTGAAGCTGCTCAGGCTTTCATGCCCTACTTCTTCAGGCTGTCGGACC 426
Qy 121 ACGGTCACAGCAGTGATTTTCAGAGATGGACAGAGCGAGCTTCATCATCAATCACTGG 180
Db 427 ACGTCAACAGTGGACTTTTCAGAGTGGAGAGCGAGCTTCATCATCAATCACTGG 486
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Db 727 TACTACGACATCTGGAATGGCTTACACGGGAACACTCTGAGCATGTTCATGCGCGC 786
Qy 481 CCTACGAAAAGAGTGCTCTCTCCGCGCTCACCAGCATCTGAGCGCTCAGCTCATC 540
Db 787 CCTATGAAAAGAGTGCTCTCTCTCCGCGCTCACCAGCATCTGAGCGCTCAGCTCATC 846
Qy 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCAGTGGAAAGGCA 862

AY889067 1209 bp mRNA linear SYN 29-MAR-2005
AY889067 Synthetic construct Homo sapiens clone FLH016840.01X serine or
DEFINITION cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
complete cds.
AY889067
ACCESSION
VERSION AY889067.1 GI:60654586

KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1209)
AUTHORS Hines,B., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and LaBaer,J.
TITLE Cloning of human full-length CDS in Creator (TM) recombinational
vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1209)
AUTHORS Hines,B., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and LaBaer,J.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using BD In-Fusion(TM) cloning system
between the SalI and HindIII sites of the pDNR-Dual vector.
Additional sequences in the clone: 'ACC' after SalI site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
clonally isolated and full-length sequence-verified.
FEATURES
Location/Qualifiers
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VLFMGQVMEP"

ORIGIN
Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
1 AAGGAGCTCATGGGCGCGTGGAAACAAGATGATCAGCACGCGCGATGCCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGCGCGTGGAAACAAGATGATCAGCACGCGCGATCTTCGTC 366
Qy 61 CAGCGGATCTGAAGCTGCTCAGGCTTTCATGCCCTACTTCTTCAGGCTGTCGGACC 120
Db 367 CAGCGGATCTGAAGCTGCTCAGGCTTTCATGCCCTACTTCTTCAGGCTGTCGGACC 426
Qy 121 ACGGTCACAGCAGTGATTTTCAGAGATGGACAGAGCGAGCTTCATCATCAATCACTGG 180
Db 427 ACGTCAACAGTGGACTTTTCAGAGTGGAGAGCGAGCTTCATCATCAATCACTGG 486
Qy 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 240

Db 487 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGACCCAG 546
QY 241 CTGACGGCGCTGTTCTGTTGAATGCGCTTACTTCAACGGCAGTGGAAAACGCCCTTC 300
Db 547 CTGACAGCGCTGGTGGTGAATGCGCTTACTTCAACGGCAGTGGAAAACGCCCTTC 606
QY 301 CCAGAGAAAAGCACTCAACCGCGCTCTTCCACAAGTCTGATGCGACGCGCTCTGTG 360
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QY 361 CCATGATGCTCAGACCAACAGTTCACACTGAGTTTCCACCCCGAGCGCCAT 420
Db 667 CCATGATGCTCAGACCAACAGTTCACACTGAGTTTCCACCCCGAGCGCCAT 726
QY 421 TACTACACATCTGGATTCCTTACCGGCACTCTGAGCATGTTTCATTCGCCGC 480
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QY 481 CCTTACAAAAGAGGTGCTCTCTCCGCGCTCACCAGCATTTGGAGCGCTCAGCTCATC 540
Db 787 CCTTACAAAAGAGGTGCTCTCTCCGCGCTCACCAGCATTTGGAGCGCTCAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCAGTGGAAAGGGA 862

RESULT 6
AY891356
LOCUS
DEFINITION
1209 bp mRNA linear SYN 21-MAR-2005
Synthetic construct Homo sapiens clone FLH031022.01L serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
partial cds.

ACCESSION
AY891356.1 GI:61369090

VERSION
Human ORF Project.

KEYWORDS
synthetic construct

SOURCE
synthetic construct

ORGANISM
other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 1209)

AUTHORS
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.

TITLE
Cloning of human full-length CDS in Creator (TM) recombinational
vector system

JOURNAL
Unpublished

REFERENCE
2 (bases 1 to 1209)

AUTHORS
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.

TITLE
Direct Submission

JOURNAL
Submitted (05-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA

COMMENT
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). The CDS has been directionally cloned using
BD In-Fusion (TM) cloning system between the Sali and HindIII sites
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
after Sali site and before 'ATG' to provide Kozak consensus
sequence; 'GG' after last codon and before HindIII site to maintain
reading frame. Each clone is clonally isolated and full-length
sequence-verified.

FEATURES
Location/Qualifiers

1..1209

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/mol_type="mRNA"

/db_xref="taxon:32630"

/clone="FLH031022.01L"

/lab_host="Escherichia coli DH5alpha TI resistant"

/note="derived from Homo sapiens first strand cDNA library

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from placenta and brain
/gene="SERPINE1"
CDS
1..>1209
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DVSPNMAOTNKNFYFTPDGHYDILELPHYGDITLSMFIAPAEKVEKPLSALTNI
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VLFMGQVMEPL"

ORIGIN

Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGACGCGCGATGCATCTTCGTG 60
Db 307 AAGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGACGCGCGATGCATCTTCGTG 366
QY 61 CAGCGGATCTGAGCTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGC 120
Db 367 CAGCGGATCTGAGCTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGC 426
QY 121 ACGTCAAGCAGTGGATTTTTCAGAGATGGACAGACGAGTTCATCATCAATGACTGG 180
Db 427 ACGTCAAGCAGTGGATTTTTCAGAGATGGACAGACGAGTTCATCATCAATGACTGG 486
QY 181 GTGAAGAGACACACAAAAGCGATGATCAATGACTTTCGCGCAAGGGCTGTGGACCAG 240
Db 487 GTGAAGAGACACACAAAAGCGATGATCAATGACTTTCGCGCAAGGGCTGTGGACCAG 546
QY 241 CTGACGCGCTGTTCTGTTGAATGCCCTTCTTCAACGGCCAGTGGAAAACGCCCTTC 300
Db 547 CTGACGCGCTGTTCTGTTGAATGCCCTTCTTCAACGGCCAGTGGAAAACGCCCTTC 606
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QY 361 CCGATGATGGCTCAGACCAACAAAGTTCACACTACATGAGTTTTCACCCCGAGCGCCAT 420
Db 667 CCGATGATGGCTCAGACCAACAAAGTTCACACTACATGAGTTTTCACCCCGAGCGCCAT 726
QY 421 TACTACGACATCTGGAATTCCTTACACGGCAACACTCTGAGCATGTTTCATTCGCCGC 480
Db 727 TACTACGACATCTGGAATTCCTTACACGGCAACACTCTGAGCATGTTTCATTCGCCGC 786
QY 481 CCTTACAAAAGAGTGGCTCTCTCCGCGCTCACCAGCATTTCTGACGCTCAGCTCATC 540
Db 787 CCTTACAAAAGAGTGGCTCTCTCTCCGCGCTCACCAGCATTTCTGAGTCCCAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCAGTGGAAAGGGA 862

RESULT 7

AY891655

LOCUS

DEFINITION

1209 bp mRNA linear SYN 29-MAR-2005

Synthetic construct Homo sapiens clone FLH016836.01L serine or

cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,

partial cds.

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ACCESSION AY891655
VERSION AY891655.1 GI:61370956
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Hines,L., Rolfs,A., Jepsen,D., Moreira,D., Raphael,J., Kelley,F.,
        Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
        Williamson,J. and Labaer,J.
TITLE Cloning of human full-length CDS in Creator (TM) recombinational
        vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1209)
AUTHORS Hines,L., Rolfs,A., Jepsen,D., Moreira,D., Raphael,J., Kelley,F.,
        Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
        Williamson,J. and Labaer,J.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular
        Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
        Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length
        expression clones generated by Harvard Institute of Proteomics.
        This ORF clone has been cloned without stop-codon (to allow fusion
        with C-terminal tag). The CDS has been directionally cloned using
        BD In-Fusion(TM) cloning system between the SalI and HindIII sites
        of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
        after SalI site and before 'ATG' to provide Kozak consensus
        sequence; 'GG' after last codon and before HindIII site to maintain
        reading frame. Each clone is clonally isolated and full-length
        sequence-verified.
FEATURES             Location/Qualifiers
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     CDS              1..>1209
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                     TVSPVMAQTKNFYETFPDGHYDILELPGHDTLSMFAAPYKEVLELSALNI
                     LSAQIISHWKNMTLRPLLVLKPSLEVDLRPLENLGMDMFRQADFTSLSD
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                     VLFMGQVMEPL"
ORIGIN
Query Match      81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGCGCGTGGACAAAGATGATGATCAGCAGCGCGATGCCATCTTCGTG 60
Db 307 AAGGAGCTCATGGCGCGTGGACAAAGATGATGATCAGCAGCGCGATGCCATCTTCGTG 366
QY 61 CAGCGGGATCTGAAGCTGTGCAGAGTTTCATGCCCTCTTCAGGCTGTTCGGACC 120
Db 367 CAGCGGGATCTGAAGCTGTGCAGAGTTTCATGCCCTCTTCAGGCTGTTCGGACC 426
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCGAGGTTCATCATCAATGACTGG 180

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Db 427 ACGGTCAAGCAGGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 486
QY 181 GTGAAGACACACACAAAAGGCATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAAG 240
Db 487 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTTGGAAAGGAGCGGTGGACCAAG 546
QY 241 CTGACGCGCCTGGTTCGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCCCTTC 300
Db 547 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCAGAGAAAAGCACTCACACCGCCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 607 CCGGACTCCAGCACCCACCGCGCCTCTTCCACAATCAGACGGCAGCACTGTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTACACTGAGTTTTCACCCCGGACGGCCAT 420
Db 667 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCCACCACCGCCGATGGCCAT 726
QY 421 TACTACGACATCTCTGGAATTGCCCTTACCAACGGCAACACTCTGAGCATGTTCATTCGCGC 480
Db 727 TACTACGACATCTCTGGAATCTGCCCTTACCAACGGGACACCCCTCAGCATGTTCATTCGCGC 786
QY 481 CCCTAGAAAAAGAGTGCCTCTCTCCGCCCTCACCAGCATCTCTGGACGCTCAGTCTCATC 540
Db 787 CTTATGAAAAAGAGTGCCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 846
QY 541 AGCCAGTCGAAAGGGA 556
Db 847 AGCCATCGAAAGGCA 862

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RESULT 8
AY893400 1209 bp mRNA linear SYN 16-MAR-2005
LOCUS AY893400
DEFINITION Synthetic construct Homo sapiens clone FLH057235.01X serine or
        cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
        complete cds.
ACCESSION AY893400
VERSION AY893400.1 GI:60817775
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Hines,L., Taron,B., Jepsen,D., Moreira,D., Raphael,J., Shen,B.,
        Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and Labaer,J.
        Cloning of human full-length CDS FLEXGene in
        Gateway(TM) recombinational vector system
        Unpublished
TITLE JOURNAL
REFERENCE 2 (bases 1 to 1209)
AUTHORS Hines,L., Taron,B., Jepsen,D., Moreira,D., Raphael,J., Shen,B.,
        Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and Labaer,J.
        Direct Submission
TITLE JOURNAL
COMMENT This CDS clone is a part of a collection of human full-length
        expression clones generated by Harvard Institute of Proteomics.
        This ORF clone has been cloned with normalized stop-codon. AttB
        recombination sites have been added to either end of the ORF and
        directionally cloned using the Gateway cloning system into pDONR
        201. Additional sequences in the clone: 'ACC' before the 'ATG'
        (corresponding to ribosomal binding site and Kozak consensus
        sequence)-verified.
        Each clone is clonally isolated and full-length
        sequence-verified.
FEATURES             Location/Qualifiers
     source           1..1209
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                     /lab_host="Escherichia coli DH5alpha T1 resistant"

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partial cds.
AY893851
Human ORF Project.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1209)
Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D., and LaBaer, J.
Cloning of human full-length CDS FLEXGene in
Gateway(TM) recombinational vector system
Unpublished
2 (bases 1 to 1209)
Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D., and LaBaer, J.
Direct Submission
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). AtB3 recombinational sites have been added to
either end of the ORF and directionally cloned using the Gateway
cloning system into pDONR 201. Additional sequences in the clone:
'ACC' before the 'ATG' (corresponding to ribosomal binding site and
Kozak consensus sequences). Each clone is clonally isolated and
full-length sequence-verified.
Location/Qualifiers
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/mol_type="mRNA"
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/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
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VLFMGQVMEP"
ORIGIN
Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGCACGGCCGATGCCAFTTCTG 60
DB 307 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGCACGGCCGATGCCAFTTCTG 366
QY 61 CAGCGGAGCTGAAGCTGTGCAGGGTTTCATGCCCTACTTCTTCAGGCTGTCCGGACC 120
DB 367 CAGCGGAGCTGAAGCTGTGCAGGGTTTCATGCCCTACTTCTTCAGGCTGTCCGGAGC 426
QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGCAGCAGGTTTCATCATCAATGACTG 180
DB 427 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGCAGCAGGTTTCATCATCAATGACTG 486
QY 181 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACCAAG 240
DB 487 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACCAAG 546
QY 241 CTGACGGCTGTTCTGTGTAATGCCCTTACTTCAACGGCCAGTGGAAAGCCGCTTC 300
DB 547 CTGACGGCTGTTCTGTGTAATGCCCTTACTTCAACGGCCAGTGGAAAGCCGCTTC 606
QY 301 CCAGAGAAAAGCACTCACACCGCTTCTCCCAAGTCTGTGATGGCAGCCGCTCTCTGTG 360
DB 607 CCGACTCCAGCACCCACCGCGCTTCTCCCAAGTCTGTGATGGCAGCCGCTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAGTTCACACTACATGAGTTTCCACCCCGCAGCGCCAT 420
DB 667 CCCATGATGGCTCAGACCAACAGTTCACACTACATGAGTTTCCACCCCGCAGCGCCAT 726
QY 421 TACTAGCATCTCTGAATGGCTTACCAACGGAACACTCTGAGCATGTTCATTCGCGCC 480
DB 727 TACTAGCATCTCTGAATGGCTTACCAACGGAACACTCTGAGCATGTTCATTCGCGCC 786
QY 481 CCTAGGAAAAGAGTGCTCTCTCCGCGCTTCCAGCATTTCTGAGCATCTGAGCTCATC 540
DB 787 CCTATGAAAAGAGTGCTCTCTCTCCGCGCTTCCAGCATTTCTGAGCATCTGAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
DB 847 AGCCAGTGGAAAGGGA 862
RESULT 9
AY893851
LOCUS
DEFINITION
AY893851 1209 bp mRNA linear SYN 16-MAR-2005
Synthetic construct Homo sapiens clone FLH057231.01L serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
CDS
ORIGIN
Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGCACGGCCGATGCCAFTTCTG 60
DB 307 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGCACGGCCGATGCCAFTTCTG 366
QY 61 CAGCGGAGCTGAAGCTGTGCAGGGTTTCATGCCCTACTTCTTCAGGCTGTCCGGACC 120
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QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGCAGCAGGTTTCATCATCAATGACTG 180
DB 427 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGCAGCAGGTTTCATCATCAATGACTG 486
QY 181 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACCAAG 240
DB 487 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACCAAG 546
QY 241 CTGACGGCTGTTCTGTGTAATGCCCTTACTTCAACGGCCAGTGGAAAGCCGCTTC 300
DB 547 CTGACGGCTGTTCTGTGTAATGCCCTTACTTCAACGGCCAGTGGAAAGCCGCTTC 606
QY 301 CCAGAGAAAAGCACTCACACCGCTTCTCCCAAGTCTGTGATGGCAGCCGCTCTCTGTG 360
DB 607 CCGACTCCAGCACCCACCGCGCTTCTCCCAAGTCTGTGATGGCAGCCGCTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAGTTCACACTACATGAGTTTCCACCCCGCAGCGCCAT 420
DB 667 CCCATGATGGCTCAGACCAACAGTTCACACTACATGAGTTTCCACCCCGCAGCGCCAT 726
QY 421 TACTAGCATCTCTGAATGGCTTACCAACGGAACACTCTGAGCATGTTCATTCGCGCC 480
DB 727 TACTAGCATCTCTGAATGGCTTACCAACGGAACACTCTGAGCATGTTCATTCGCGCC 786
QY 481 CCTAGGAAAAGAGTGCTCTCTCCGCGCTTCCAGCATTTCTGAGCATCTGAGCTCATC 540
DB 787 CCTATGAAAAGAGTGCTCTCTCTCCGCGCTTCCAGCATTTCTGAGCATCTGAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
DB 847 AGCCAGTGGAAAGGGA 862
RESULT 9
AY893851
LOCUS
DEFINITION
AY893851 1209 bp mRNA linear SYN 16-MAR-2005
Synthetic construct Homo sapiens clone FLH057231.01L serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,

Db 427 ACGGTCAAGCAAGTGAGCTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 486
Qy 181 GTGAAGAGACACACAAAAGGCATGATCAATGACTTTTCTGTCGCAAGGGCTGCTGGACCCAG 240
Db 487 GTGAAGACACACACAAAAGGTATGATCAGCACTTCTTGGAAAAGGAGCCGTGGACCCAG 546
Qy 241 CTGACGCGCTGGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAACGCCCTTC 300
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Db 727 TACTACGACATCCTGGAATGCCCTTACACGGCAACACTCTGAGCATGTTCAATTCGCCGC 786
Qy 481 CCCTAGAAAAGAGGTGCTCTCTCGGCCCTACACAGCATTTCTGGAAGCTCAGCTCATC 540
Db 787 CTTATGAAAAGAGGTGCTCTCTCTCGGCCCTACACAAATCTCTGAGTGCCAGCTCATC 846
Qy 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCACTGGAAAGGCA 862

RESULT 10
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DEFINITION Sequence 2218 from Patent WO02068579.
ACCESSION CQ716284
VERSION CQ716284.1 GI:42277141
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
JOURNAL Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
PE Corporation (NY) (US)
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ORIGIN
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Besc Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGATCAGCAGCGGCCCATGTCATCTTCGTG 60
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Db 813 CCATGATGGCTCAGACCAACAAGTTCAACTACACTGAGTTTTCACACCCCGACGCCCAT 872
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RESULT 11
LOCUS HSPAIR1 1962 bp mRNA linear PRI 27-MAR-1995
DEFINITION Human mRNA for plasminogen activator inhibitor (PAI-1).
ACCESSION X04744
VERSION X04744.1 GI:35275
KEYWORDS glycoprotein; plasminogen activator inhibitor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE Hominidae; Homo.
JOURNAL Wun, T.C. and Kretzmer, K.K.
PE Corporation (NY) (US)
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Query Match 81.9%; Score 455.2; DB 8; Length 1962;
Best Local Similarity 88.7%; Pred. No. 1 6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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Qy 121 ACGGTCAAGCAGGTGGATTTTCAGAGATGAGACAGACGAGTTCATCATCAATGACTGG 180
Db 379 ACGGTCAAGCAGGTGGATTTTCAGAGATGAGACAGACGAGTTCATCATCAATGACTGG 438
Qy 181 GTCAAGAGACACAAAGGATGATCAATGACTTCTTGGCCAAAGGGGCTGTGGACCCAG 240
Db 439 GTCAAGAGACACAAAGGATGATCAATGACTTCTTGGCCAAAGGGGCTGTGGACCCAG 498
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Qy 541 AGCCAGTGGAAAGGGA 556
Db 799 AGCCACTGGAAAGGCA 814

RESULT 12
LOCUS BC010860
DEFINITION Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1, mRNA (cDNA clone MGC:9226 IMAGE:3893914), complete cds.
ACCESSION BC010860
VERSION BC010860.1 GI:14790035
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2207)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Collins,K.H., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smillius,D.E., Schnerk,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2207)
NIH MGC Project
Direct Submission
Submitted (12-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTP/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 14 Row: 9 Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835158.

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Query Match 81.9%; Score 455.2; DB 8; Length 2207;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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LOCUS CO413075 2660 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 20146 from Patent WO0170979.
ACCESSION CO413075
VERSION CO413075.1 GI:41320856
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 20146 27-SEP-2001;
FEATURES Millennium Pharmaceuticals, Inc. (US)
source Location/Qualifiers
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Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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LOCUS AR106060 2876 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6103498.
ACCESSION AR106060
VERSION AR106060.1 GI:12820125
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2876)
AUTHORS Lawrence, D.A. and Stefansson, S.P.
TITLE Mutant plasminogen activator-inhibitor type 1 (PAI-1) and uses thereof
JOURNAL Patent: US 6103498-A 1 15-AUG-2000;
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Best Local Similarity 88.7%; Pred. No. 1.6e-96;
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DEFINITION Sequence 10 from patent US 6103498.
ACCESSION AR106066
VERSION AR106066.1 GI:12820131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2876)
AUTHORS Lawrence,D.A. and Stefansson,S.P.
TITLE Mutant plasminogen activator-inhibitor type 1 (PAI-1) and uses thereof
JOURNAL Patent: US 6103498-A 10 15-AUG-2000;
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Best Local Similarity 88.7%; Pred. No. 1.6e-96;
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Searched: 4996997 seqs, 3332346308 residues

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Listing first 45 summaries

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4: Geneseq2001as.*
5: Geneseq2001bs.*
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14: Geneseq2005s.*

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8	455.2	81.9	1962	10	ACF79499	Human p
9	455.2	81.9	2016	13	ACN41744	Human d
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35	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
36	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
37	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
38	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
39	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
40	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
41	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
42	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
43	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
44	455.2	81.9	2876	14	AE81038	Ae81038 Human lym
45	455.2	81.9	2876	14	AE81038	Ae81038 Human lym

ALIGNMENTS

RESULT 1
ACF79497
ID ACF79497 standard; CDNA; 2970 BP.
XX
AC ACF79497;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cattle plasminogen activator inhibitor-1 cDNA.
XX
KW Plasminogen activator inhibitor-1; PAI-1; cattle; transgenic;
KW thrombolytic; antiasthmatic; antiinflammatory; neutropic;
KW neuroprotective; antidepressant; nephrotropic; vulnary;
KW antiseborrheic; dermatological; antiarteriosclerotic; hepatotropic;
KW gene; ss.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
CDS 122..1330
FT /*tag= a
FT /product= "Cattle PAI-1"
XX
PN WO2003071267-A1.
XX
PD 28-AUG-2003.
XX
PF 19-FEB-2003; 2003WO-US005008.
XX
PR 19-FEB-2003; 2002US-0358061P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PA (DECL/) DECLERCK P J.
XX
PI Declerck PJ, Vaughan DE, Eren M;
XX
DR WPI; 2003-721694/68.
XX
DR P-PSDB; ABR63122.
XX
PT Treating a warm-blooded vertebrate animal having a medical condition,
PT e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or
PT glomerulosclerosis, comprises administering a plasminogen activator

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGSGCTGTTCCGGACC 120
DB 649 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGSGCTGTTCCGGACC 708
QY 121 ACGTCAAGCAAGTGGATTTTTCAGAGATGGACAGCAGCGGTTTCATCAATCAATGACTGG 180
DB 709 ACGTCAAGCAAGTGGATTTTTCAGAGATGGACAGCAGCGGTTTCATCAATCAATGACTGG 768
QY 181 GTGAGAGACACACAAAAGGATCATCAATGACTTACTTGGCCAAAGGGCTGTGGACAG 240
DB 769 GTGAGAGACACACAAAAGGATCATCAATGACTTACTTGGCCAAAGGGCTGTGGACAG 828
QY 241 CTGACGGCTGGTCTGGTGAATGCGCTCTACTTCAAGCCAGTGGAAAAGCGCCCTTC 300
DB 829 CTGACGGCTGGTCTGGTGAATGCGCTCTACTTCAAGCCAGTGGAAAAGCGCCCTTC 888
QY 301 CCAGAGAAAAGCACTACACCGCTCTTCCACAAGTCTGATGGCAGCAGCGTCTCTGTG 360
DB 889 CCGACTCCAGCACCCACCGCTCTTCCACAAGTCTGATGGCAGCAGCGTCTCTGTG 948
QY 361 CCATGATGCTGACACCAAGTTCACACTGAGTTTCCACCCCGAGCGGCAT 420
DB 949 CCATGATGCTGACACCAAGTTCACACTGAGTTTCCACCCCGAGCGGCAT 1008
QY 421 TACTAGACATCTGGATTCGCTTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCC 480
DB 1009 TACTAGACATCTGGATTCGCTTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCC 1068
QY 481 CCTTACGAAAAGAGTGGCTCTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCC 540
DB 1069 CCTTATGAAAAGAGTGGCTCTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCCAGCTCATC 1128
QY 541 AGCCAGTGGAAAAGGA 556
DB 1129 AGCCAGTGGAAAAGGA 1144

RESULT 3

ID ADQ38429
XX ADQ38429 standard; DNA; 3320 BP.
AC ADQ38429;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 92.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; gene; db.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
XX WPI; 2004-533949/51.
DR P-PSDB; ADQ39257.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in

the individual's nucleic acids.

Claim 7; SEQ ID NO 92; 145pp; English.

PT
XX
PS
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting a SNP in a
CC nucleic acid molecule; a method of detecting a Variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

Sequence 3320 BP; 825 A; 879 C; 828 G; 759 T; 0 U; 29 Other;

Query Match 82.1%; Score 456.4; DB 13; Length 3320;

Best Local Similarity 88.1%; Pred. No. 6.9e-111;

Matches 490; Conservative 5; Mismatch 61; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGCAGCGCCGATGTCATCTTCGTG 60
DB 589 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGCAGCGCCGATGTCATCTTCGTG 648
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC 120
DB 649 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC 708
QY 121 ACGTCAAGCAAGTGGATTTTTCAGAGATGGACAGCAGCGGTTTCATCATCATGACTGG 180
DB 709 ACGTCAAGCAAGTGGATTTTTCAGAGATGGACAGCAGCGGTTTCATCATCATGACTGG 768
QY 181 GTGAGAGACACACAAAAGGATCATCAATGACTTACTTGGCCAGGGCTGTGGACCCAG 240
DB 769 GTGAGAGACACACAAAAGGATCATCAATGACTTACTTGGCCAGGGCTGTGGACCCAG 828
QY 241 CTGACGGCTGGTCTGGTGAATGCGCTCTACTTCAAGCCAGTGGAAAAGCGCCCTTC 300
DB 829 CTGACGGCTGGTCTGGTGAATGCGCTCTACTTCAAGCCAGTGGAAAAGCGCCCTTC 888
QY 301 CCAGAGAAAAGCACTACACCGCTCTTCCACAAGTCTGATGGCAGCAGCGTCTCTGTG 360
DB 889 CCGACTCCAGCACCCACCGCTCTTCCACAAGTCTGATGGCAGCAGCGTCTCTGTG 948
QY 361 CCATGATGCTGACACCAAGTTCACACTGAGTTTCCACCCCGAGCGGCAT 420
DB 949 CCATGATGCTGACACCAAGTTCACACTGAGTTTCCACCCCGAGCGGCAT 1008
QY 421 TACTAGACATCTGGATTCGCTTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCC 480
DB 1009 TACTAGACATCTGGATTCGCTTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCC 1068
QY 481 CCTTACGAAAAGAGTGGCTCTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCC 540
DB 1069 CCTTATGAAAAGAGTGGCTCTCTCCCGCTTCCACGAGCACTCTGAGCATGTTTCATGCGCCAGCTCATC 1128

QY 541 AGCCAGTGGAAAGGGA 556
Db 1129 AGCCACTGGAAAGGCA 1144

RESULT 4
ADF28770
ID ADF28770 standard; cDNA; 1209 BP.
XX AC ADF28770;
XX DT 12-FEB-2004 (first entry)
XX DE Human plasminogen-activator inhibitor-1 (PAI-1) encoding cDNA.
XX KW Urokinase-type plasminogen activator; uPA;
KW plasminogen-activator inhibitor-1; PAI-1; breast cancer; tumour;
KW cancer therapy; human; ss; gene.
XX OS Homo sapiens.
XX FH Key
FT CDS
FT 1..1209
FT /*tag= a
FT /product= "PAI-1"
FT /note= "plasminogen activator inhibitor type 1"

WO2003082072-A2.
XX PN
XX PD 09-OCT-2003.
XX PF 13-FEB-2003; 2003WO-US004538.
XX PR 13-FEB-2002; 2002US-035928P.
PR P-PSDB; ADF28771.
XX (HARB/) HARBECK N.
PA (KATE/) KATES R E.
PA (SCHM/) SCHMITT M.
PA (FOEK/) FOEKENS J A.
XX PI Harbeck N, Kates RE, Schmitt M, Foekens JA;
XX WPI; 2003-803930/75.
DR P-PSDB; ADF28771.
XX
PT Selecting treatments for cancer, specifically breast cancer, based on
PT levels of urokinase and plasminogen-activator inhibitor-1 in tissue.
XX
PS Disclosure; SEQ ID NO 3; 133pp; English.
XX
CC The invention relates to selecting a treatment regime with highest
CC expected benefit to a patient with primary breast cancer. The method
CC involves measuring the levels of urokinase-type plasminogen activator
CC (uPA) and plasminogen-activator inhibitor-1 (PAI-1), or corresponding
CC mRNA, in primary tumour tissue (or a sample); and classifying the patient
CC as low risk (LR) if the uPA level is below a cut-off value of between the
CC 55 th . and 75 th percentile of normalized or analogous uPA in a
CC randomized population of breast cancer patients, and if the PAI-1 level
CC is lower than a cut-off value between the 61 st and 81 st percentile in
CC the same population, or as high risk (HR) if the levels of uPA and PAI-1
CC are above these cut-off values. The treatment of LR (or HR) patients is
CC then selected as one that results in the highest expected benefit in a
CC comparable population of LR (or HR) patients. The method is used: for
CC selection of the most effective therapy, including one designed to
CC prevent relapse; and to predict expected benefit, overall or disease-free
CC survival in patients with cancer, particularly of the breast but also
CC leukemia and plasmacytoma. The method can also be used; to predict the
CC benefit of preventative treatment for relapse of cancer, especially where
CC HR patients are treated with bisphosphonate drugs; for deciding whether
CC or not to administer an aggressive or non-aggressive regime; and for
CC deciding whether or not to administer chemotherapy in combination with

CC hormone therapy (i.e. if the patient is LR, chemotherapy is not
CC administered; in this case HR patients are those who are estrogen- and/or
CC progesterone- receptor positive). The present sequence represents a cDNA
CC encoding a human PAI-1 polypeptide.
XX
SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 10; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCCTGGAAACAAAGATGATGATCAGCACGGCGATGCCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGGCCATGGAAACAAAGATGATGATCAGCACGACGATCTTCGTG 366
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 120
Db 367 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGAGC 426
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGAGCCAGGTTTCATCATCAATGACTGG 180
Db 427 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGAGCCAGGTTTCATCATCAATGACTGG 486
QY 181 GTGAAGAGACACACAAAAGGCAATGATCAATGATTTCTTGGCCAAAGGGCTGTGGACCCAG 240
Db 487 GTGAAGAGACACACAAAAGGATATGATCAGCAACTTGTCTGGGAAAGGAGCCGTGGACCCAG 546
QY 241 CTGACGGCGCTGGTTCTGGTGAATGCCCTCTACTTCAAGCGCCAGTGGAAAGCGCCCTTC 300
Db 547 CTGACAGCGCTGGTGGTGAATGCCCTCTACTTCAAGCGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCAGAGAAAAAGCACTCACACCGCCTCTTCCACAAAGTCTGTATGGCAGACACCGCTCTCTGTG 360
Db 607 CCCGACTCCAGCACCCACCGCGCCTCTTCCACAAATCAGACGGCAGACATGTCTCTGTG 666
QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACATCTGATTTTTCACCCCGACGGCCAT 420
Db 667 CCATGATGGCTCAGACCAACAAAGTTCAACTATATCTAGATTCCACCACGCCCGATGCCAT 726
QY 421 TACTAGGACATCTTGAATTCGCCCTTACCACGGCACATCTGAGCATGTTCATTCGGCC 480
Db 727 TACTAGGACATCTTGAATTCGCCCTTACCACGGGGACACCCCTCAGCATGTTCATTCGGCC 786
QY 481 CCTACGAAAAAGAGGTGCTCTCTCCGCCCTTCCACGACATCTCGACGCTCAGCTCATC 540
Db 787 CCTATGAAAAAGAGGTGCTCTCTCTGCCCTTCCACCAACATCTCTAGTGGCCAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCACTGGAAAGGCA 862

RESULT 5
AAD64654
ID AAD64654 standard; cDNA; 1209 BP.
XX AC AAD64654;
XX DT 12-FEB-2004 (first entry)
XX DE Human plasminogen activator inhibitor-1 (PAI-1) coding region.
XX KW Plasminogen activator inhibitor-1; PAI-1; cardiovascular disease;
KW fibrotic disease; gene therapy; antiinflammatory; gene; human; ss.
XX OS Homo sapiens.
XX FH Key
FT CDS
FT 1..1209
FT /*tag= a
FT /product= "Human plasminogen activator inhibitor-1
FT protein"
FT /note= "Capital T represents cleavage sites"

Db	847	AGCCTGGAAAGGCA	862
RESULT 6			
ADV42563			
ID	ADV42563	standard; cDNA; 1209 BP.	
XX	XX		
XX	AC	ADV42563;	
XX	XX		
DT	10-MAR-2005	(first entry)	
XX	XX		
DE	Human psychoneuroendocrinimmune	expressed sequence tag SEQ ID NO 191.	
XX	XX		
KW	microarray; psychoneuroendocrinimmune;	chronic fatigue;	
KW	non-insulin dependent diabetes; allergy;	immune disorder; inflammation;	
KW	cancer; neoplasm; infection;	expressed sequence tag; ss.	
XX	XX		
OS	Homo sapiens.		
XX	XX		
FN	W02004108899-A2.		
XX	XX		
PD	16-DEC-2004.		
XX	XX		
PF	04-JUN-2004; 2004WO-US017686.		
XX	XX		
PR	04-JUN-2003; 2003US-0475915P.		
XX	XX		
PA	(USSH.) US DEPT HEALTH & HUMAN SERVICES.		
XX	XX		
PI	Nicholson A., Vernon SD;		
PI	PI		
XX	XX		
DR	WPI; 2005-031682/03.		
XX	XX		
PT	New microarray comprising probes for genes involved in		
PT	psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a		
PT	condition associated with PNI activity, e.g., inflammatory or infectious		
PT	diseases.		
XX	XX		
XX	Claim 1; SEQ ID NO 191; 254pp; English.		
PS	XX		
CC	The invention relates to a new microarray which comprises probes for		
CC	genes involved in psychoneuroendocrinimmune (PNI) activity. The		
CC	microarray is useful in diagnosing a condition associated with PNI		
CC	activity, such as CFS, type-2 diabetes, allergic condition, inflammation,		
CC	cancer and infection. The present sequence represents a		
CC	psychoneuroendocrinimmune gene expressed sequence tag. Note the		
CC	specificatio mentions SEQ ID NO of up to 3314 but only sequences up to		
CC	SEQ ID NO 1829 are provided.		
XX	XX		
SQ	Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;		
Query Match	81.9%;	Score 455.2; DB 14; Length 1209;	
Best Local Similarity	88.7%;	Pred. No. 1e-110;	
Matches	493; Conservative	0; Mismatches 63; Indels 0; Gaps 0	
QY	1	AAGGAGCTCATGGGCGTCGACACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60	
Db	307	AAGGAGCTCATGGGCGCATGGAAACAGGATGAGATCAGCAGCGCGATCTTCGTC 366	
QY	61	CAGCGGATCTGAAGCTGGTTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 120	
Db	367	CAGCGGATCTGAAGCTGGTTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 426	
QY	121	ACGGTCAAGCAGTGGATTTTTTCAGAGATGGACAGCCAGGTTTCATCAATCAATGACTGG 180	
Db	427	ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 486	
QY	181	GTCAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAAAGGGGTGTGGACAG 240	
Db	487	GTCAAGAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGGACCAG 546	
QY	241	CTGACGCGCTGGTCTCTGGTGAATGCCCTCTACTTCAACGCGCCAGTGGAAAACGCCCTTC 300	

Db 547 CTGACACGGCTGGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 606
QY 301 CCAGAGAAAAGCACTCACCACCGCCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 607 CCGGACTCCAGACCCACCGCGCCTCTTCCAAATCAGACGGGAGCACTGTCTGTG 666
QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTTTTCACCCCGGAGCCAT 420
Db 667 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTTTTCACCCCGGAGCCAT 726
QY 421 TACTAGGACATCTGGAATTCCTTACACGGCAGCACTCTGAGCATGTTCTATTCGGCC 480
Db 727 TACTAGGACATCTGGAATTCCTTACACGGCAGCACTCTGAGCATGTTCTATTCGGCC 786
QY 481 CCTACGAAAAGAGTGCTCTCTCCGCCCTCACCAGCATTTCTGACGCTCAGTCTCATC 540
Db 787 CTTTATGAAAAGAGTGCTCTCTCTGCCCTCACCAGCATTTCTGAGTGCCAGTCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCACTGGAAAGGCA 862

RESULT 7
AEA81050
ID AEA81050 standard; cDNA; 1209 BP.
XX
AC AEA81050;
XX
DT 08-SEP-2005 (first entry)
DE Human plasminogen activator inhibitor-1 encoding cDNA SEQ ID NO:17.
XX
KW antisense therapy; RNA interference; plasminogen activator inhibitor-1;
KW vasotrophic; thrombolytic; hemostatic; vascular disease;
KW thrombocyte disorder; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..1209
FT /*tag= a
FT /product= "plasminogen activator inhibitor-1 (PAI-1)"
XX
FN US2005148527-A1.
XX
PD 07-JUL-2005.
XX
PF 24-FEB-2005; 2005US-00512496.
XX
PR 23-APR-2002; 2002US-00128706.
PR 23-APR-2003; 2003WO-US012767.
XX
XX (ITES/) ITESCU S.
PA
XX
PI Itescu S;
XX
DR WPI: 2005-478099/48.
DR P-PSDB; AEA81039.
XX

New catalytic nucleic acid that specifically cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1), useful for treating vascular, thrombotic or hemostatic disorders.

Disclosure; SEQ ID NO 17; 53pp; English.

XX
XX The invention relates to a catalytic nucleic acid that specifically cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1).
XX Also described: (1) a pharmaceutical composition comprising the catalytic nucleic acid, oligonucleotide, or inhibitor of PAI-1 expression, and a carrier; (2) a method of treating a cardiovascular disease in a subject; (3) a method of treating a vascular disease in a subject where the disease is treated by reducing thrombin or fibrin production; (4) a

CC method of treating a vascular disease in a subject where the vascular disease is treated by inhibition of PAI-1 expression; (5) a method of inducing neovascularization in a heart tissue of a subject; (6) a method of inhibiting smooth muscle cell proliferation in a tissue of a subject; (7) a method of inhibiting thrombin and fibrin deposition in a heart or tissue of a subject; (8) a method of treating a subject suffering from a thrombotic disease or disorder, or hemostatic disorder where the disease or disorder is associated with elevated expression of PAI-1; and (9) a method of treating a disorder of a subject's heart involving loss of cardiomyocytes. The nucleic acid, compositions and methods are useful for treating vascular, thrombotic or hemostatic disorders. The present sequence encodes human PAI-1, which is used in the exemplification of the present invention.

XX
SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;

Query Match 81.9%; Score 455.2; DB 14; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCGCTGGAAACAAAGATGAGATCAGCAGCGCGATGCCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGGCCCATGGAACAAAGATGAGATCAGCAGCGCGATCTTCGTG 366
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 120
Db 367 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGAGC 426
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGATGAGCAGAGCAGGTTTCATCATCAATGACTGG 180
Db 427 ACGGTCAAGCAGGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTCATCAATGACTGG 486
QY 181 GTGAAGACACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGCACCA 240
Db 487 GTGAAGACACACACAAAGGATGATCAGCAACTTGTGGAAAGAGCGGTGACACCA 546
QY 241 CTGACGCGCTGGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCCCTTC 300
Db 547 CTGACAGCGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCAGAAAAGCACTCACCACCGCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 607 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTTTTCACCCCGGAGCCCAT 420
Db 667 CCCATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTTTTCACCCCGGAGCCCAT 726
QY 421 TACTACGACATCTTGGAAATTCCTTACACGGCAGCACTCTGAGCATGTTTCATTCGGCC 480
Db 727 TACTACGACATCTTGGAAATTCCTTACACGGGAGCACCCCTCAGCATGTTTCATTCGCTG 786
QY 481 CCCTACGAAAAGAGGTGCTCTCTCCGCCCTCACCAGCATTTCTGAGCGCTCAGTCTCATC 540
Db 787 CTTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCAGCATTTCTGAGTGCCAGTCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCACTGGAAAGGCA 862

RESULT 8
ACF79499
ID ACF79499 standard; cDNA; 1962 BP.
XX
AC ACF79499;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human plasminogen activator inhibitor-1 partial cDNA.
XX Plasminogen activator inhibitor-1; PAI-1; human; transgenic;
KW thrombolytic; antiasthmatic; antiinflammatory; nootropic;

KW neuroprotective; antidepressant; nephrotropic; vulnary;
KW antiseborrheic; dermatological; antiarteriosclerotic; hepatotropic;
KW gene; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1161
FT /*tag= a
FT /partial
FT /product= "Human PAI-1"
FT /note= "No start codon"
XX
XX WO2003071267-A1.
XX
XX 28-AUG-2003.
XX
XX 19-FEB-2003; 2003WO-US005008.
XX
XX 19-FEB-2002; 2002US-0358061P.
XX
XX (UYVA-) UNIV VANDERBILT.
XX (DECL/) DECLERCK P J.
XX
XX Declerck PJ, Vaughan DE, Eren M;
XX
XX WPI: 2003-721694/68.
XX P-PSDB; ABR63124.
XX
XX Treating a warm-blooded vertebrate animal having a medical condition,
XX e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or
XX glomerulosclerosis, comprises administering a plasminogen activator
XX inhibitor-1 inhibitor.
XX
XX Disclosure; Page 64-66; 91pp; English.
XX
XX The present sequence is that a partial cDNA for human plasminogen
XX activator inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce
XX transgenic animals of the invention, useful for screening potential PAI-1
XX inhibitors. Such PAI-1 inhibitors can be used to treat a warm-blooded
XX vertebrate animal having a medical condition, e.g. alopecia, undesired
XX weight loss, Alzheimer's disease, systemic amyloidosis, myelofibrosis,
XX glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne,
XX atherosclerosis, ageing, or a wound (claimed). A method of testing a
XX candidate composition for PAI-1 inhibition activity comprises
XX administering the composition to a transgenic animal having a PAI-1 gene
XX incorporated into its genome, and observing an ameliorating change in the
XX animal indicative of inhibition of PAI-1 activity, the change being an
XX improvement of a vascular thrombotic disorder, asthma, chronic
XX obstructive pulmonary disease, alopecia, undesired weight loss such as
XX anorexia, Alzheimer's disease, systemic amyloid deposition, systemic
XX amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness,
XX keloids, apocrine cysts, acne, atherosclerosis, ageing,
XX hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
XX
XX Sequence 1962 BP; 456 A; 569 C; 505 G; 432 T; 0 U; 0 Other;
XX
XX Query Match 81.9%; Score 455.2; DB 10; Length 1962;
XX Best Local Similarity 88.7%; Pred. No. 1.2e-110;
XX Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
XX
XX 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGGT 60
XX 259 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGGT 318
XX
XX 61 CAGCGGATCTGAAGCTGTTCAGGCTTCATGCCCTTCTTCAGGCTGTTCGGAC 120
XX
XX 319 CAGCGGATCTGAAGCTGTTCAGGCTTCATGCCCTTCTTCAGGCTGTTCGGAGC 378
XX
XX 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGGACAGGCGAGGTTCATCATCAATCACTGG 180
XX 379 ACGGTCAAGCAGGTGATTTTTCAGAGATGGAGGCGAGGTTCATCATCAATCACTGG 438
XX

QY 181 GTCAAGAGACACACAAAAGGCATGATCAATGACTTACTTGGCCCAAGGGCTGTGGACCA 240
DB 439 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGACCGTGGACCA 498
QY 241 CTGACGCGCTGCTTCTGTGTAATGCTTACTTCAACGCGCAGTGGAAAACGCCCCCTTC 300
DB 499 CTGACACGGCTGCTGTGTAATGCTTACTTCAACGCGCAGTGGAAAGATCCCTTC 558
QY 301 CCAGAGAAAAGCACTCACCACCGCTCTTCCCAAAGTCTGATGGCAGCACCGTCTCTGTG 360
DB 559 CCGGACTCCAGCACCCACCGCGCTCTTCCCAAATCAGACGGCAGCAGTCTCTGTG 618
QY 361 CCCATGATGCTCAGACCAACCAAGTTCAACTACACTGAGTTTCCACCCCGAGGCGCAT 420
DB 619 CCCATGATGCTCAGACCAACCAAGTTCAACTACACTGAGTTTCCACCGCGATGGCCAT 678
QY 421 TACTACGACATCTCGAAATTTGCCCTACCAAGCAACACTCTGAGCATGTTTCATTGGCGCC 480
DB 679 TACTACGACATCTCGAAATTTGCCCTACCAAGCAACACTCTGAGCATGTTTCATTGGCGCC 738
QY 481 CCTACGAAAAGAGTGGCTCTCTCGGCTCACCAGCATTTGGAAGCTCAGCTCATC 540
DB 739 CCTTATGAAAAGAGTGGCTCTCTCGGCTCACCAGCATTTGGAAGCTCAGCTCATC 798
QY 541 AGCCAGTGGAAAGGA 556
DB 799 AGCCACTGGAAAGGA 814
RESULT 9
ACN41744
ID ACN41744 standard; cDNA; 2016 BP.
XX
XX ACN41744;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:619.
DE ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW dithp.
XX
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
XX Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
XX Patry S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
XX P-PSDB; AEM93092.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 1; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2016 BP; 464 A; 628 C; 508 G; 416 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 13; Length 2016;
Best Local Similarity 88.7%; Pred. No. 1.2e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGGAACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
Db |||||
QY 61 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGACC 120
Db |||||
QY 489 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGAGC 548
Db |||||
QY 121 ACGGTCAGCAGCTGATTTTTCAGAGATGGACAGCGCTTCATCATCAATCACTGG 180
Db |||||
QY 549 ACGGTCAGCAGCTGATTTTTCAGAGATGGAGAGCGAGATTCATCATCAATCACTGG 608
Db |||||
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGACCA 240
Db |||||
QY 609 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTTGGGAAGAGGCGTGGACCA 668
QY 241 CTGACGGCTGTGGTCTGATGATGCTTCTACTTCAACGGGCTGTGAAACGCGCTTC 300
Db |||||
QY 669 CTGACAGGGCTGTGGTCTGATGATGCTTCTACTTCAACGGGCTGTGAAAGACTCCCTTC 728
QY 301 CCAGAGAAAGCACTCACCGCTCTTCCACAGTCTGATGGCAGCACGCTCTCTGTG 360
Db |||||
QY 729 CCGGACTCAGCAGCCACCGCGCTCTTCCAAATCAGAGGCGAGCACTGTCTGTG 788
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACCCCGACGCCAT 420
Db |||||
QY 789 CCGATGATGGCTCAGACCAACAAAGTTCAACTATCTGAGTTTTCACCAACCGCGATGCCAT 848
QY 421 TACTACGATCTCTGGAATGCGCTTACCAACGCAACACTCTGAGCATGTTCAATTCGCGC 480
Db |||||
QY 849 TACTACGATCTCTGGAATGCGCTTACCAACGCGGACACCTCTGAGCATGTTCAATTCGCGC 908
QY 481 CCTACGAAAGAGGTGCTCTCTCCGCTTCCAGCATCTGAGCGCTCAGCTCATC 540
Db |||||
QY 909 CTTTATGAAAGAGGTGCTCTCTCTGCTTCCAAATCTGAGTGCGCCAGCTCATC 968
QY 541 AGCCAGTGGAAAGGGA 556
Db |||||
QY 969 AGCCACTGGAAGGCA 984
RESULT 10
ID ACN41743
XX ACN41743 standard; cDNA; 2053 BP.
XX ACN41743;
AC ACN41743;
XX
DT 18-NOV-2004 (first entry)
XX

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:618.
XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW dithp.
XX Homo sapiens.
XX WO2004023973-A2.
XX 25-MAR-2004.
XX 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EU, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
DR P-FSDB; ABW83091.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2053 BP; 471 A; 642 C; 512 G; 428 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 13; Length 2053;
Best Local Similarity 88.7%; Pred. No. 1.2e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGGAACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
Db |||||
QY 61 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGACC 120
Db |||||
QY 526 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGAGC 585
QY 121 ACGGTCAGCAGCTGATTTTTCAGAGATGGACAGCGCTTCATCATCAATCACTGG 180
Db |||||
QY 586 ACGGTCAGCAGCTGATTTTTCAGAGATGGAGAGCGAGATTCATCATCAATCACTGG 645
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGACCA 240

CC	mammal. The method is useful in treating a mammal having a tumor of glial
CC	origin comprising cells that express a type A or B glial tumor antigen.
CC	This sequence represents a human tumor-associated antigenic target
CC	polynucleotide.
XX	
SQ	Sequence 2177 BP; 515 A; 638 C; 553 G; 471 T; 0 U; 0 Other;
	Query Match 81.9%; Score 455.2; DB 14; Length 2177;
	Best Local Similarity 88.7%; Pred.No. 1.3e-110;
	Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY	1 AAGGAGCTCATGGGCGGTGAAACAAAGATCAGATCAGCAGCGCGATGCCATCTTCGTG 60
Db	414 AAGGAGCTCATGGGCGCATGGAAACAGATGAGATCAGACACAGACGCGATCTTCGTG 473
QY	61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTCCGGACC 120
Db	474 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCATCTTCTTCAGGCTGTTCGGAGC 533
QY	121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
Db	534 ACGGTCAAGCAGGTGGATTTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 593
QY	181 GTGAAGAGACACAAAGGCATGATCAATGACTTACTTGGCCCAAGGGGCTGTGGACCAG 240
Db	594 GTGAAGAGACACAAAGGCATGATCAATGACTTACTTGGCCCAAGGGGCTGTGGACCAG 240

		241	CTGACGGCCTGGTCTTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAAAGCCCTTC	300
QY				
		654	CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC	713
Db				
		301	CCAGAGAAAAGCACTCACCAACCGCCTTTTCCACAAGTCTGATGGCAGCACCGCTCTCTGTG	360
QY				
		714	CCCGACTCCAGCACCCACACCGCGCCTCTTCCACAAATCAGACGCGCAGCACTGTCTCTGTG	773
Db				
		361	CCCATGATGGCTCAGACCAACAAGTTTCAACTACACTGAGTTTTCACACCCCGCAGCGCCAT	420
QY				
		774	CCCATGATGGCTCAGACCAACAAGTTTCAACTATACTGAGTTTCAACACGCCCGGATGGCCAT	833
Db				
		421	TACTACGACATCCTGGAAATTGGCCCTACCAACGGCAACACTCTGAGCATGTTTCAATTCGCCCC	480
QY				
		834	TACTACGACATCCTGGAAATTGGCCCTACCAACGGGACACCCCTCAGCATGTTTCAATTCGCTGCC	893
Db				
		481	CCCTACGAAAAAGAGTGCCTCTCTCGCCCTCACACAGCAATTCGGACGCTCAGCTCATC	540
QY				
		894	CCTTATGAAAAAGAGTGCCTCTCTCGCCCTCACCAACAATTCGAGTGCCAGCTCATC	953
Db				
		541	AGCCAGTGGAAAGGGA	556
QY				
		954	AGCCACTGGAAAGGCA	969
Db				

RESULT 12	
ADL61934	
ID	ADL61934 standard; DNA; 2660 BP.
XX	
AC	ADL61934;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Human ovarian cancer DNA marker #20146.
XX	
KW	Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX	
OS	Homo sapiens.
XX	
PN	WO200170979-A2.
XX	
PD	27-SEP-2001.
XX	
PF	21-MAR-2001; 2001WO-US009126.
XX	
XX	21-MAR-2000; 2000US-0191031P.
PR	

PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 20146; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
SQ Sequence 2660 BP; 615 A; 799 C; 653 G; 593 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 5; Length 2660;
Best Local Similarity 88.7%; Pred. No. 1.3e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGCGCGTGGGAACAAAGATGATGATCAGCAGCGCGCATCTTCGTG 60
DB 452 AAGGAGCTCATGGCGCGCATGGGAACAAAGATGATGATCAGCAGCGCGCATCTTCGTG 511
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
DB 512 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 571
QY 121 ACGGTCAGCAGCGTGAATTTTCAGAGATGGAAGCAGCAGCGGTTTCATCATCAATCACTGG 180
DB 572 ACGGTCAGCAGCGTGAATTTTCAGAGATGGAAGCAGCAGCGGTTTCATCATCAATCACTGG 631
QY 181 GTGAGAGACACACAAAAGGCATGATCAATGATCTTACTTGGCCAGGGCTGTGACCCAG 240
DB 632 GTGAGAGACACACAAAAGGCATGATCAATGATCTTACTTGGCCAGGGCTGTGACCCAG 691
QY 241 CTGACGCGCGCTGGTCTTGTTGAATGCTCCCTCTACTTCAACGCGCAGTGGAAAAACGCCCTTC 300

DB 692 CTGACACGCTGGTGGTGAATGCCCTTACTTTCAACGGCCAGTGGGAAGACTCCCTTC 751
QY 301 CCAGAGAAAAGCACTCAGCAGCGCTCTTCCAAAGTCTGATGGCAGCAGCCGCTCTCTGTG 360
DB 752 CCCGACTCCAGCAGCCAGCGCGCTCTTCCAAATCAGAGCGGAGCAGCTGTCTCTGTG 811
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTCCACCCCGCAGCGCCAT 420
DB 812 CCCATGATGGCTCAGACCAACAAAGTTCAACTATATCTAGTTTCCACCGCCGATGGCCAT 871
QY 421 TACTACGACATCTTGAATTTGCCCTTACCAAGCAACTCTGAGCATGTTTCAATTCGCGCC 480
DB 872 TACTACGACATCTTGAATTTGCCCTTACCAAGCAACTCTGAGCATGTTTCAATTCGCGCC 931
QY 481 CCCTACGAAAAGAGGTGCTCTCTCCGCCCTCACCAGCATCTTGGACGCTCAGCTCATC 540
DB 932 CTTTATGAAAAGAGGTGCTCTCTCTGCCCTTCCAAACATTTGAGTGCCCGAGCTCATC 991
QY 541 AGCCAGTGGAAAGGGA 556
DB 992 AGCCACTGGAAAGGCA 1007
RESULT 13
ID ABV94750 standard; cDNA; 2870 BP.
XX AC ABV94750;
XX DT 14-JAN-2003 (first entry)
DE Human pancreatic cancer expressed cDNA SEQ ID NO 131.
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
OS Homo sapiens.
XX WO200260317-A2.
PD 08-AUG-2002.
XX 30-JAN-2002; 2002WO-US002781.
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI WPI; 2002-627435/67.
XX P-PSDB; ABP68605.
DR
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 131; 300pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity

to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match.	81.9%;	Score 455.2;	DB 6;	Length 2870;
Best Local Similarity	88.7%;	Pred. No. 1.4e-110;		
Matches 493;	Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;
QY	1	AAGGAGCTCATGGGCGCTGGACAAAGATCAGATCAGCAGCGCGGATGCCATCTTGTCG	60	
Db	376	AAGGAGCTCATGGGCGCATGACAAAGATGAGATCAGACCAAGAGCGGATCTTGTC	435	
QY	61	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGCGTGTTCGGGACC	120	
Db	436	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCACCTTCTTCAGCGTGTTCGGGACC	495	
QY	121	ACGGTCAAGCAGGTGGATTTTCAGAGATGGACAGAGCGAGGTTCATCAATGACTGG	180	
Db	496	ACGGTCAAGCAGGTGGACTTTTCAGAGGTGGAGAGCGAGATTCATCAATGACTGG	555	
QY	181	GTGAAGAGACACACAAAGGCATGATCAATGACTTTCTTGCCCAAGGGCTGTGGACCA	240	
Db	556	GTGAAGACACACAAAGGTATGATCAGCACTTGTGTGGAAAGAGCGGTGGACCA	615	
QY	241	CTGACGGCTGGTTCTGGTGAATGCCCTCTACTTCAACGCGCAGTGGAAAACGCCCTTC	300	
Db	616	CTGACAGCGTGGTGGTGAATGCCCTCTACTTCAACGCGCAGTGGAAAACGCCCTTC	675	
QY	301	CCAGAGAAAGCACTCACACCGCCTCTCCACAAGTCTGATGGCAGCAGCTCTGTG	360	
Db	676	CCGCACTCAGCAACCCACACCGCGCCTCTCCACAATCAGACGGCAGCACTGTCTGTG	735	
QY	361	CCCATGATGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGCAGGCGCAT	420	
Db	736	CCCATGATGCTCAGACCAACAAAGTTCAACTATCTGAGTTTCACCGCCCGATGGCCAT	795	
QY	421	TACTACGATCTCTGGAAATGGCCCTTACCAAGCAACACTCTGAGCAATGTTCAITGGCGCC	480	
Db	796	TACTACGATCTCTGGAACTGCCCTTACCAAGGGAACACCTTCAGCATGTTCAITGTGCC	855	
QY	481	CCCTACGAAAAGAGTGGCTCTCTCGGCCCTCACCAGCAATCTGGACGCTCAGCTCATC	540	
Db	856	CCTTATGAAAAGAGTGGCTCTCTCTGCCCTCACCACATCTTGAGTGGCCAGCTCATC	915	
QY	541	AGCCAGTGGAAAGGGA	556	
Db	916	AGCCACTGGAAGGCA	931	

RESULT 14	
AAT97303	
ID	AAT97303 standard; DNA; 2876 BP.
XX	
XX	AAT97303;
XX	
XX	
DT	14-APR-1998 (first entry)
XX	
XX	
DE	Human plasminogen activator inhibitor DNA.
DE	
XX	
XX	Plasminogen activator inhibitor type 1; PAI-1; human; elastase inhibitor;
KW	vitronectin; cell attachment; cell migration; cell proliferation;
KW	emphysema; adult respiratory distress syndrome; acute lung inflammation;
KW	

KW	alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis;
KW	pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis;
KW	restenosis; neointima; fibrosis; wound healing; tumour; metastasis;
KW	psoriasis; thrombosis; angiogenesis; therapy; ds.
OS	Homo sapiens.
XX	
FH	Key
XX	Location/Qualifiers
FT	CDS
FT	76..1284
FT	/*tag= a
FT	sig_peptide
FT	76..144
FT	/*tag= b
FT	mat_peptide
FT	145..1281
FT	/*tag= c
XX	
XX	
PN	W09739028-A1.
XX	
XX	
PD	23-OCT-1997.
XX	
XX	
PF	11-APR-1997; 97WO-US0606071.
XX	
XX	
PR	12-APR-1996; 96US-0015299P.
XX	
XX	(AMNA-) AMERICAN NAT RED CROSS.
PA	
XX	
XX	
PI	Lawrence DA, Stefansson SP;
XX	
XX	
DR	WFI; 1997-526399/48.
DR	P-PDSB; AAW31587.
XX	
XX	
PT	Plasminogen activator-inhibitor type I mutant inhibits elastase - or has
PT	high affinity for vitronectin, for therapeutic inhibition of elastase or
PT	vitronectin-mediated cell attachment, migration etc.
XX	
XX	
PS	Disclosure; Page 91-95; 144pp; English.

CC This nucleotide sequence codes for wild-type human plasminogen activator
CC inhibitor type (PAI-1) (see AAW31587). Novel mutants (see AAW26710-25) of
CC the PAI-1 mature protein are claimed that inhibit elastase or other
CC elastase-like proteases, or are inhibitors of vitronectin-dependent cell
CC migration. The mutants are obtained by site-directed mutagenesis of the
CC PAI-1 DNA sequence and expression in host cells, and have a range of
CC therapeutic uses.

Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;

Query Match	81.9%	Score 455.2	DB 2	Length 2876
Best Local Similarity	88.7%	Pred. No. 1.4e-110		
Matches 493	Conservative	0	Mismatches 63	Indels 0
			Gaps 0	

1	AAAGAGCTCATGGGGCCGTGGAA	CAAAAGATGAGATCAGCACGCCGATGCATCTTCGTG	60
382	AAAGAGCTCATGGGGCCATGAA	CAAGGATGAGATCAGCACCGCATCTTCGTC	441
61	CAGCCGGGATCTGAAGCTGGTCCAGGGTT	CATGCCCTACTTCTTCAGGCTGTCCGGACC	120
442	CAGCCGGGATCTGAAGCTGGTCCAGGGTT	CATGCCCACTTCTTCAGGCTGTTCGGGAGC	501
121	ACGGTCAAGCAGGTGGATTTTT	CAGAGATCGACAGCAGGTTCAATCAATGACTGG	180
502	ACGGTCAAGCAAGTGGACTTTT	CAGAGGTCAGAGAGCCAGATTCAATCAATGACTGG	561
181	GTGAAGACACACAAAGGCGATGATCAATGA	CTTACTTGGCCAAAGGGGCTGTGGACCAG	240
562	GTGAAGACACACAAAGGATGATCAGCAA	CTTGCTTGGGAAAGAGAGCCGTGGHACAG	621
241	CTGACGCGCCTGGTTCTGGTGAATGCCCTCT	ACTTTCAAAGCCGACAGTGGAAAAAGCCGCTTTC	300
622	CTGACACGGCTGGTGGTGAATGCCCTCT	ACTTTCAAAGCCGACAGTGGHAGACTCCCTTTC	681
301	CCAGAGAAAAAGCATCACACCGGCTCTTCCA	AAAGTCTGAATGGCAGCACCGGCTCTCTGTG	360
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QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACACCCCGACGGCCAT 420
Db 742 CCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACACCGCCGATGGCCAT 801
QY 421 TACTAGGACATCCTGGAATTCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGGCC 480
Db 802 TACTAGGACATCCTGGAATTCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGGCC 861
QY 481 CCCTACGAAAAAGAGTGCTCTCTCCGGCCCTCACCAGCATTTCTGGACGCTCAGCTCATC 540
Db 862 CTTATGAAAAAGAGTGCTCTCTCTGCGCTTACCAACACTTCTGAGTCCCGAGTCTATC 921
QY 541 AGCCAGTGGAAAGGGA 556
Db 922 AGCCACTGGAAAGGCA 937
RESULT 15
ID AAS09460 standard; cDNA; 2876 BP.
XX AAS09460;
AC AAS09460;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human cDNA encoding Plasminogen activator inhibitor-1, PAI-1.
XX
KW Human; Plasminogen activator inhibitor-1; PAI-1; serpin;
KW immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome;
KW ARDS; HIV infection; Human immunodeficiency virus; prostate cancer;
KW TNF-mediated inflammation; benign prostatic hypertrophy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 76..1284
FT /tag= a
FT /product= "PAI-1"
FT sig_peptide 76..143
FT /tag= c
FT /note= "Alternative signal peptide"
FT sig_peptide 76..138
FT /tag= b
FT /note= "Alternative signal peptide"
FT mat_peptide 139..1281
FT /tag= d
FT /label= Mature PAI_1 #1
FT /note= "Both forms of the protein are detected in vivo"
FT mat_peptide 144..1281
FT /tag= e
FT /label= Mature PAI_1 #2
FT /note= "Both forms of the protein are detected in vivo"
XX
PN WO200138560-A2.
XX
XX 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032315.
XX
XX 22-NOV-1999; 99US-0167553P.
XX
XX (AMNA-) AMERICAN NAT RED CROSS.
XX
XX Lawrence DA, Day D;
PI
DR WPI; 2001-441438/47.
DR P-PSDB; AAU04913.
XX
XX Detecting a functionally active form of an enzyme in a biological sample
XX comprises contacting an enzyme inhibitor immobilized on a solid
XX substrate.
XX

PS Disclosure; Fig 3; 69pp; English.
XX The sequence encodes human plasminogen activator inhibitor-1, PAI-1, a
CC serine proteinase inhibitor or serpin. The protein is used to demonstrate
CC the method of the invention which comprises detecting a functionally
CC active form of an enzyme in a biological sample by contacting an enzyme
CC inhibitor immobilised on a solid substrate with the biological sample and
CC measuring the binding of the enzyme inhibitor to the active form of the
CC enzyme by a detectable label, where the enzyme inhibitor specifically
CC forms a covalent bond or binds with a dissociation constant of 1 x 10⁻⁹M
CC or less with the active form of the enzyme. The present invention
CC provides a sensitive method for the detection of a functionally active
CC form of an enzyme in a biological sample. Human PAI-1 can be used to
CC detect a number of enzymes including tissue plasminogen activator,
CC urokinase, thrombin, plasmin, neutrophil elastase, pancreatic elastase,
CC trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as
CC such can be used in methods to diagnose diseases such as cystic fibrosis,
CC acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated
CC inflammation, prostate cancer and benign prostatic hypertrophy
XX
SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 4; Length 2876;
Best Local Similarity 88.7%; Fred. No. 1.4e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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Db 382 AAGGAGCTCATGGGGCCGCTGGAAACAAAGATGAGATCAGACAGCGCGATCTTCGTG 441
QY 61 CAGCGGAGATCGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTTCAGGCTGTTCGGGACC 120
Db 442 CAGCGGAGATCGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTTCAGGCTGTTCGGGAGC 501
QY 121 ACGGTCAACGAGGTGGATTTTTCAGATGAGACAGACAGCGAGCTTCATCATCAATCACTGG 180
Db 502 ACGGTCAACGAGGTGGATTTTTCAGAGGTGGAGAGAGCCAGATTCATCAATCACTGG 561
QY 181 GTGAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGCTCTGGACCAAG 240
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QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCCCGACGGCCAT 420
Db 742 CCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCGCCGATGGCCAT 801
QY 421 TACTACGACATCTCTGGAATTCGCCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGGCC 480
Db 802 TACTACGACATCTCTGGAATTCGCCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGGCC 861
QY 481 CCCTACGAAAAAGAGTGCTCTCTCCGGCCCTCACCAGCATTTCTGGACGCTCAGCTCATC 540
Db 862 CTTATGAAAAAGAGTGCTCTCTCTGCGCTTACCAACACTTCTGAGTCCCGAGTCTATC 921
QY 541 AGCCAGTGGAAAGGGA 556
Db 922 AGCCACTGGAAAGGCA 937
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Job time : 475.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:40 ; Search time 141.5 Seconds
(without alignments)
6984.624 Million cell updates/sec

Title: US-10-686-428A-3_COPY_444_999

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfilesi.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	455.2	81.9	2876	3	US-08-840-204-1
2	455.2	81.9	2876	3	US-08-840-204-1
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4	455.2	81.9	2876	3	US-09-324-494A-10
5	455.2	81.9	2876	3	US-09-023-655-1187
6	98.6	17.7	1191	3	US-09-016-434-1210
7	98.6	17.7	2029	9	5495001-6
8	97	17.4	2029	9	5187089-1
9	97	17.4	2029	9	5457090-1
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12	97	17.4	2032	9	5457090-3
13	74.8	13.5	1564	3	US-08-948-997-1
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28	72.6	13.1	1152	6	PCT-US95-12509-13
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ALIGNMENTS

RESULT 1
US-08-840-204-1
; Sequence 1, Application US/08840204
; Patent No. 6103498
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: STEFANSSON, STEINGRIMUR P.
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
; TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,204
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 30807-20004:00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; NAME/KEY: CDS
; LOCATION: 76..1281
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 145
; FEATURE:

NAME/KEY: sig_peptide
LOCATION: 76..144
US-08-840-204-1

Query Match 81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

1 AAGGAGCTCATGGGGCGGTGGAAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 60
382 AAGGAGCTCATGGGGCGGTGGAAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 441

61 CAGCGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTCTTCAAGCTGTTCGGAGC 120
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682 CCGACTCCAGCACCACCGCGCTTCTTCCAAATCAGACGGCAGCACTGTCTGTG 741

361 CCATGATGGCTCAGACCAAGTTCAACTACCTGAGTTTTCACCCCGCAGCGCCAT 420
742 CCATGATGGCTCAGACCAAGTTCAACTACCTGAGTTTTCACCCCGCAGCGCCAT 801

421 TACTACGATCTTGGAAATTCCTTACACGGCCACACTCTGAGCATGTTCAATTCGGCC 480
802 TACTACGATCTTGGAAATTCCTTACACGGCCACACTCTGAGCATGTTCAATTCGGCC 861

481 CCTACGAAAGAGTGCTCTCTCCGCTTCCAGCAATTCAGCACTGTGAGCTCATC 540
862 CCTATGAAAGAGTGCTCTCTTGCCTTCCACCAATCTGAGTCCCGAGCTCATC 921

541 AGCCAGTGGAAAGGGA 556
922 AGCCACTGGAAGGCA 937

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30807-20004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-840-204-10

Query Match 81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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361 CCGATGATGGCTCAGACCAAGTTCAACTACCTGAGTTTTCACCCCGCAGCGCCAT 420
2135 CCGATGATGGCTCAGACCAAGTTCAACTACCTGAGTTTTCACCCCGCAGCGCCAT 2076

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2075 TACTACGATCTTGGAAATTCCTTACCGCAGCACTCTGAGCATGTTCAATTCGGCC 2016

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2015 CCTATGAAAGAGTGCTCTCTTGCCTTCCACCAATCTGAGTCCCGAGCTCATC 1956

541 AGCCAGTGGAAAGGGA 556
1955 AGCCACTGGAAGGCA 1940

RESULT 3
US-09-324-494A-1
Sequence 1, Application US/09324494A
Patent No. 6489143
GENERAL INFORMATION:
APPLICANT: LAWRENCE, Daniel A
APPLICANT: STEFANSON, Steingrimumur P
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THEREOF
FILE REFERENCE: 30523/167

US-08-840-204-10/c
Sequence 10, Application US/08840204
Patent No. 6103498
GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSON, STEINGRIMUMUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204

; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1281)
; OTHER INFORMATION:
; US-09-324-494A-1

Query Match 81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGCATGCCATCTTCGTG 60
DB 382 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGCATCTTCGTG 441
QY 61 CAGCGGATCTGAAGCTGCTCCAGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAC 120
DB 442 CAGCGGATCTGAAGCTGCTCCAGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAC 501
QY 121 ACAGTCAAGCAGTGGATTTTCAGAGATGAGACGCGCGCATCTTCATCAATGACTGG 180
DB 502 ACAGTCAAGCAGTGGATTTTCAGAGATGAGACGCGCGCATCTTCATCAATGACTGG 561
QY 181 GTGAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGAC 240
DB 562 GTGAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGAC 621
QY 241 CTGACGCGCTGTGTTCTGGTGAATGCGCTTCTTCAAGCGCGAGTGGAAACGCGCTTC 300
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QY 301 CCAGAGAAAGCACTACCAACCGCTTCTTCCAAAGTCTGATGGACGCGCTCTCTGTG 360
DB 682 CCGGACTCCAGCACCCACCGCGCTTCTTCCAAATCAGACGCGCGCATCTCTGTG 741
QY 361 CCATGATGCTCAGACCAAGTTCACACTAGTGTTCACCGCGCGCATCTCTGTG 420
DB 742 CCATGATGCTCAGACCAAGTTCACACTAGTGTTCACCGCGCGCATCTCTGTG 801
QY 421 TACTAGCATCTCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 480
DB 802 TACTAGCATCTCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 861
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DB 862 CCTATGAAAAGAGTGCTCTCTCTGCGCTTCCAGCATTTGAGTGCCAGCTCATC 921
QY 541 AGCCAGTGAAGGGA 556
DB 922 AGCCACTGGAAGGCA 937

RESULT 4

US-09-324-494A-10/c
; Sequence 10, Application US/09324494A
; Patent No. 6489143
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, Daniel A
; APPLICANT: STEFANSON, Steingrur P
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
; FILE REFERENCE: 30523/167
; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10

; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-324-494A-10

Query Match 81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGCATGCCATCTTCGTG 60
DB 2495 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGCATCTTCGTG 2436
QY 61 CAGCGGATCTGAAGCTGCTCCAGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAC 120
DB 2435 CAGCGGATCTGAAGCTGCTCCAGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAC 2376
QY 121 ACAGTCAAGCAGTGGATTTTCAGAGATGAGACGCGCGCATCTTCATCAATGACTGG 180
DB 2375 ACAGTCAAGCAGTGGATTTTCAGAGATGAGACGCGCGCATCTTCATCAATGACTGG 2316
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DB 2315 GTGAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGAC 2256
QY 241 CTGACGCGCTGTGTTCTGGTGAATGCGCTTCTTCAAGCGCGAGTGGAAACGCGCTTC 300
DB 2255 CTGACGCGCTGTGTTCTGGTGAATGCGCTTCTTCAAGCGCGAGTGGAAACGCGCTTC 2196
QY 301 CCAGAGAAAGCACTACCAACCGCTTCTTCCAAAGTCTGATGGACGCGCTCTCTGTG 360
DB 2195 CCGGACTCCAGCACCCACCGCGCTTCTTCCAAATCAGACGCGCGCATCTCTGTG 2136
QY 361 CCATGATGCTCAGACCAAGTTCACACTAGTGTTCACCGCGCGCATCTCTGTG 420
DB 2135 CCATGATGCTCAGACCAAGTTCACACTAGTGTTCACCGCGCGCATCTCTGTG 2076
QY 421 TACTAGCATCTCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 480
DB 2075 TACTAGCATCTCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 2016
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DB 2015 CCTATGAAAAGAGTGCTCTCTCTGCGCTTCCAGCATTTGAGTGCCAGCTCATC 1956
QY 541 AGCCAGTGAAGGGA 556
DB 1955 AGCCACTGGAAGGCA 1940

RESULT 5

US-09-023-655-1187
; Sequence 1187, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1187:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2876 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g189541
/ US-09-023-655-1187

Query Match      81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGGAACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
DB 382 AAGGAGCTCATGGGCGGTGGGAACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 441

QY 61 GAGCGGATCTCAAGCTGTCTCAGGGTTTCATGCCCTTCTTCAAGCTGTTCGGGACC 120
DB 442 GAGCGGATCTCAAGCTGTCTCAGGGTTTCATGCCCTTCTTCAAGCTGTTCGGGACC 501

QY 121 ACGGTCAAGCAGTGTGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
DB 502 ACGGTCAAGCAGTGTGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 561

QY 181 GTGAAGAGACACACAAAAGGCGATGATCAATGACTTCTTGGCCAAAGGGCTGTGGACCAG 240
DB 562 GTGAAGAGACACACAAAAGGCGATGATCAATGACTTCTTGGCCAAAGGGCTGTGGACCAG 621

QY 241 CTGACGCGCTGTGTCTGTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAGCGCCCTTC 300
DB 622 CTGACGCGCTGTGTCTGTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAGCGCCCTTC 681

QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCAAAGTCTGTAGGGCAGCAGCTCTCTGTG 360
DB 682 CCGGACTCCAGACACCCACCGCGCTCTTCCAAATCAGAGCGGAGCACTGTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCCCGCAGCGCCAT 420
DB 742 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCGCGCAGTGGCCAT 801

QY 421 TACTACGACATCCTGGAATGCGCTTACCAAGCAACACTCTGAGCATGTTCAATGCGGCC 480
DB 802 TACTACGACATCCTGGAATGCGCTTACCAAGCAACACTCTGAGCATGTTCAATGCGGCC 861

QY 481 CCCTACGAAAAGAGTGGCTCTCTCCGCTCAGCAGCATTTTCGAGCGCTCAGCTCATC 540
DB 862 CTTTATGAAAAGAGTGGCTCTCTCTGCGCTCAGCAGCATTTTCGAGCGCTCAGCTCATC 921

QY 541 AGCCAGTGGAAAGGCA 556
DB 922 AGCCACTGGAAGGCA 937
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RESULT 6

US-09-016-434-1210

5

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/ Sequence 1210, Application US/09016434
/ Patent No. 6500938
/ GENERAL INFORMATION:
/ APPLICANT: Janice Au-Young
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
/ TITLE OF INVENTION: PATHWAY GENE EXPRESSION
/ NUMBER OF SEQUENCES: 1490
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,434
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0002 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1210:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1191 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g183063
/ US-09-016-434-1210
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Query Match      17.7%; Score 98.6; DB 3; Length 1191;
Best Local Similarity 49.9%; Pred. No. 7.2e-18;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

QY 1 AAGGAGCTCATGGGCGGTGGGAACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
DB 289 AAGGCGCATCGTCTCAAGAAGAAATAAGACATTTGTGACAGTGGCTAACCGCGTGTGTT 348

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 120
DB 349 AAGATGCTCTGAATTTGAATGCTCTTTGTACAGGAACAAGATGTTGTTCCAGTGT 408

QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
DB 409 GAGGTCCGGAATGTGAACCTTTGAGGATCCAGCCTCTGCTGTGATTCATCAATGACTGG 468

QY 181 GTGAAGAGACACACAAAAGGCGATGATCAATGACTTACTTGGCCAGGGGCTGTGGACCA- 239
DB 469 GTTAAAAACGAAACAGGGATATGATTGACAAATCTGCTGTCCCCAGATCTTTATTGATGGT 528

QY 240 --GCTGCGCGCTGTGTTCTGTTGAATGCCCTCTACTTCAACGGCCAGTGGAAAAACGCC 297
DB 529 GTGCTCAGACACTGCTCTCTGTAACGCGAGTGTATTTCAAGGGTCTGTGGAAATCAGCG 588

QY 298 TTCCCGAGAGAAAAGCACTCACACCGCTCTTTCACAAAGTCTGATGGCAGCACCGCTCTCT 357
DB 589 TTCCAAACCGGAGAACACAAAGAAACGCACTTTTCGTGGCAGCGCGGAAATCTCTATCAA 648
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QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCACACTACAGTGGTTCACACCCCGCAGGC 417
DB 649 GTGCCAATGCTGGCCAGCTCTCCGTTCCGGTGTGGGTGCAACAAGTGGCCCAATGAT 708
QY 418 CATTACTACGACATCTCTGGAAATTCCTTACACGGCAACACTCTGAGCATGTTCAATGGC 477
DB 709 TTATGTTACAACTTCATTGAATGACCTCCCTACACGGGAAGCATCAGCATGCTGATTTGA 768
QY 478 GCCCCTTACGAAAGAGGTGCTCTCTCCGCTCACCAGCATTTCTGGAGCTCAGCTC 537
DB 769 CTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCAGCAACCAAGCC 828
QY 538 ATCAGCCAGTGA 550
DB 829 ATAGACAGCTGA 841

RESULT 7
5495001-6
; Patent No. 5495001
; APPLICANT: MCGROGAN, MICHAEL P.; SCOTT, RANDY W.; BAKER,
; JOFFRE B.; SIMONSEN, CHRISTIAN C.
; TITLE OF INVENTION: RECOMBINANT PURIFIED PROTEASE NEXIN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,596
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 111,111
; FILING DATE: 24-AUG-1993
; APPLICATION NUMBER: 25,450
; FILING DATE: 13-MAR-1987
; APPLICATION NUMBER: 871,501
; FILING DATE: 06-JUN-1986
; APPLICATION NUMBER: 870,232
; FILING DATE: 03-JUN-1986
; SEQ ID NO: 6:
; LENGTH: 2029
5495001-6

Query Match 17.7%; Score 98.6; DB 9; Length 2029;
Best Local Similarity 49.9%; Pred. No. 8.8e-18;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;
QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
DB 433 AAGGCCATCGTCTCCAAAGAGATAAAGACATTGTGACAGTGGCTAAGCCGTTTGT 492
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCAGCCCTACTTTCTCAGGCTGTTCCGGACC 120
DB 493 AAGAATGCTCTGAAATTTGAAGTGCCTTTTGTACAAAGAAACAAAGATGTTCCAGTGT 552
QY 121 ACGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCATGACTGG 180
DB 553 GAGTCCGGAAATGTGAATTTGAGGATCCAGCTCTGCTGTGATTCATCAATGATG 612
QY 181 GTCAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGAC- 239
DB 613 GTTAAACACGAAACACAGGATATGATTGACATCTCTGCTCCACAGATCTTATGATGT 672
QY 238 CAGCTGACGCGCTGGTCTGGTGAATGCCCTTACTTCAACGGCCAGTGGAAACGCCC 297
DB 673 GTGCTCACCAGACTGGTCTCGTCAACGCGAGTGTATTTCAAGGGTCTGTGGAAATCAGG 732
QY 298 TTCCAGAGAAAGCACTCACCACCGCTTTCACCAAGTCTGATGGCAGCACCGTCTCT 357
DB 733 TTCCAAACCCGAGAACACAAAGAAACGCACTTTCTGGGAGCCGACGGGAAATCTATCAA 792
QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCACACTACAGTGTTCACACCCCGCAGGC 417
DB 793 GTGCCAATGCTGGCCAGCTCTCCGTTCCGGTGTGGGTTCGACAGTGGCCCAATGAT 852
QY 418 CATTACTACGACATCTCTGGAAATTCCTTACACGGCAACACTCTCTGAGCATGTTCAATGGC 477
DB 853 TTATGTTACAACTTCATTGAATGACCTCCCTACACGGGAAGCATCAGCATGCTGATTTGA 912
QY 478 GCCCCTTACGAAAGAGGTGCTCTCTCCGCTCACCAGCATTTCTGGAGCTCAGCTC 537
DB 733 TTCCAAACCCGAGAACACAAAGAAACGCACTTTCTGGGAGCCGACGGGAAATCTATCAA 792
QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCACACTACAGTGTTCACACCCCGCAGGC 417
DB 793 GTGCCAATGCTGGCCAGCTCTCCGTTCCGGTGTGGGTTCGACAGTGGCCCAATGAT 852

RESULT 9

QY 418 CATTACTACGACATCTCTGGAAATTCCTTACACGGCAACACTCTGAGCATGTTCAATGGC 477
DB 853 TTATGTTACAACTTCATTGAATGACCTCCCTACACGGGAAGCATCAGCATGCTGATTTGA 912
QY 478 GCCCCTTACGAAAGAGGTGCTCTCTCCGCTCACCAGCATTTCTGGAGCTCAGCTC 537
DB 913 CTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCAGCAACCAAGCC 972
QY 538 ATCAGCCAGTGA 550
DB 973 ATAGACAGCTGA 985
RESULT 8
5187089-1
; Patent No. 5187089
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-1 VARIANTS WHICH INHIBIT
; ELASTASE
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 1:
; LENGTH: 2029
5187089-1

Query Match 17.4%; Score 97; DB 9; Length 2029;
Best Local Similarity 49.7%; Pred. No. 2.5e-17;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;
QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
DB 433 AAGGCCATCGTCTCCAAAGAGATAAAGACATTGTGACAGTGGCTAAGCCGTTTGT 492
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCAGCCCTACTTTCTCAGGCTGTTCCGGACC 120
DB 493 AAGAATGCTCTGAAATTTGAAGTGCCTTTTGTACAAAGAAACAAAGATGTTCCAGTGT 552
QY 121 ACGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCATGACTGG 180
DB 553 GAGTCCGGAAATGTGAATTTGAGGATCCAGCTCTGCTGTGATTCATCAATGATG 612
QY 181 GTCAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGAC- 237
DB 613 GTTAAACACGAAACACAGGATATGATTGACATCTCTGCTCCACAGATCTTATGATGT 672
QY 238 CAGCTGACGCGCTGGTCTGGTGAATGCCCTTACTTCAACGGCCAGTGGAAACGCCC 297
DB 673 GTGCTCACCAGACTGGTCTCGTCAACGCGAGTGTATTTCAAGGGTCTGTGGAAATCAGG 732
QY 298 TTCCAGAGAAAGCACTCACCACCGCTTTCACCAAGTCTGATGGCAGCACCGTCTCT 357
DB 733 TTCCAAACCCGAGAACACAAAGAAACGCACTTTCTGGGAGCCGACGGGAAATCTATCAA 792
QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCACACTACAGTGTTCACACCCCGCAGGC 417
DB 793 GTGCCAATGCTGGCCAGCTCTCCGTTCCGGTGTGGGTTCGACAGTGGCCCAATGAT 852
QY 418 CATTACTACGACATCTCTGGAAATTCCTTACACGGCAACACTCTCTGAGCATGTTCAATGGC 477
DB 853 TTATGTTACAACTTCATTGAATGACCTCCCTACACGGGAAGCATCAGCATGCTGATTTGA 912
QY 478 GCCCCTTACGAAAGAGGTGCTCTCTCCGCTCACCAGCATTTCTGGAGCTCAGCTC 537
DB 913 CTGCGGACTGAGAGTTCACACTCCGCTGTCTGCCATCATCCACACATCAGCAACCAAGCC 972
QY 538 ATCAGCCAGTGA 550
DB 973 ATAGACAGCTGA 985

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5457090-1
; Patent No. 5457090
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,294
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO:1
; LENGTH: 2029
;
Query Match
Best Local Similarity 17.4%; Score 97; DB 9; Length 2029;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
Db 432 AAGGCCATCGTCTCAAGAAGAAATAAGACATTTGACAGTGGCTAAACGCGTGTGTT 491
QY 61 CAGCGGATCTGAAGTGTTCAGGTTTCAATGCTTCTTCAAGGAAACAAAGATGTGTCCAGTGT 120
Db 493 AAGGATGCTCTGAAATGAAGTGCCTTTTGTACAAAGGAAACAAAGATGTGTCCAGTGT 552
QY 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGAGACAGCGCAGGTTCATCATCAATCACTGG 180
Db 553 GAGGTCCGAATGTGAATTTTTCAGAGATGAGACAGCGCAGGTTCATCATCAATCACTGG 612
QY 181 GTGAAGAGACACACAAAGGCAATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGAC--- 237
Db 613 GTTAAAAACGAAACCCAGGATATGATGACATCTGCTGCCAGATCTTATTGATGT 672
QY 238 CAGCTGACCGGCTGTGTTCTGATGATGCTTCTTCAAGCGGCAAGTGGGAAACGCCC 297
Db 673 GTGCTCACCAGACTGTCTCTGCTCAACGAGTGTATTTTCAAGGGTCTGTGGAATCAAG 732
QY 298 TTCCCGAGAGAAAGCACTCACCACCGCTTCCCAAGTCTGTGAGGAGCAGCCGCTCT 357
Db 733 TTCCCAACCCGAGAACAAAGAAACGCACTTTCTGTCGAGCGGAGCGGAAATCCTATCAA 792
QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCAACTACACTAGTGTTCACACCCCGACGGC 417
Db 793 GTGCCAATGCTGGCCAGCTCTCCGTGTTCCGGTGTGGTGCACAGTGCCTCCCATGAT 852
QY 418 CATTACTAGCATCTCTGGAATTCCTTACCAACGCAACACTCTCAGCATGTTTCAATGCC 477
Db 853 TTATGTTACAACTTCAATGAACTGCTTCAACGAGTGTATTTTCAAGGGTCTGTGGAATCAAG 912
QY 478 GCGCCCTACGAAAGAGGTGCTCTCTCCGCTTCCAGCAACACTCTCAGCATGTTTCAATGCC 537
Db 913 CTGCGAGTGTGAGGTCCACTCCGCTGTCTGCCATCATCCACATCAGCAGCAAGACC 972
QY 538 ATCAGCCAGTGA 550
Db 973 ATAGACAGTGA 985

RESULT 10
5495001-8
; Patent No. 5495001
; APPLICANT: MCGROGAN, MICHAEL P.; SCOTT, RANDY W.; BAKER,
; JOFFRE B.; SIMONSEN, CHRISTIAN C.
; TITLE OF INVENTION: RECOMBINANT PURIFIED PROTEASE NEXIN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,596
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 111,111
; FILING DATE: 24-AUG-1993
;
Query Match
Best Local Similarity 17.4%; Score 97; DB 9; Length 2032;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;
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5495001-8
; APPLICATION NUMBER: 25,450
; FILING DATE: 13-MAR-1987
; APPLICATION NUMBER: 871,501
; FILING DATE: 06-JUN-1986
; APPLICATION NUMBER: 870,232
; FILING DATE: 03-JUN-1986
; SEQ ID NO:8
; LENGTH: 2031
;
Query Match
Best Local Similarity 17.4%; Score 97; DB 9; Length 2031;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
Db 432 AAGGCCATCGTCTCAAGAAGAAATAAGACATTTGACAGTGGCTAAACGCGTGTGTT 491
QY 61 CAGCGGATCTGAAGTGTTCAGGTTTCAATGCTTCTTCAAGGAAACAAAGATGTGTCCAGTGT 120
Db 492 AAGGATGCTCTGAAATGAAGTGCCTTTTGTACAAAGGAAACAAAGATGTGTCCAGTGT 551
QY 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGAGACAGCGCAGGTTCATCATCAATCACTGG 180
Db 552 GAGGTCCGAATGTGAATTTTTCAGAGATGAGACAGCGCAGGTTCATCATCAATCACTGG 611
QY 181 GTGAAGAGACACACAAAGGCAATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGAC--- 237
Db 612 GTTAAAAATGAACCCAGGATATGATGACATCTGCTGCCAGATCTTATTGATGT 671
QY 238 CAGCTGACCGGCTGTGTTCTGATGATGCTTCTTCAAGCGGCAAGTGGGAAACGCCC 297
Db 672 GTGCTCACCAGACTGTCTCTGCTCAACGAGTGTATTTTCAAGGGTCTGTGGAATCAAG 731
QY 298 TTCCCGAGAGAAAGCACTCACCACCGCTTCCCAAGTCTGTGAGGAGCAGCCGCTCT 357
Db 732 TTCCCAACCCGAGAACAAAGAAACGCACTTTCTGTCGAGCGGAGCGGAAATCCTATCAA 791
QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCAACTACACTAGTGTTCACACCCCGACGGC 417
Db 792 GTGCCAATGCTGGCCAGCTCTCCGTGTTCCGGTGTGGTGCACAGTGCCTCCCATGAT 851
QY 418 CATTACTAGCATCTCTGGAATTCCTTACCAACGCAACACTCTCAGCATGTTTCAATGCC 477
Db 852 TTATGTTACAACTTCAATGAACTGCTTCAACGAGTGTATTTTCAAGGGTCTGTGGAATCAAG 911
QY 478 GCGCCCTACGAAAGAGGTGCTCTCTCCGCTTCCAGCAACACTCTCAGCATGTTTCAATGCC 537
Db 912 CTGCGAGTGTGAGGTCCACTCCGCTGTCTGCCATCATCCACATCAGCAGCAAGACC 971
QY 538 ATCAGCCAGTGA 550
Db 972 ATAGACAGTGA 984

RESULT 11
5187089-3
; Patent No. 5187089
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT
; ELASTASE
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO:3
; LENGTH: 2032
;
Query Match
Best Local Similarity 17.4%; Score 97; DB 9; Length 2032;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;
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QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
DB 433 AAGGCCATCGTCTCCRAAGAAATAAGACATTTGTGACAGTGGCTAACGCCGTGTTGTT 492
QY 61 CAGGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTACTTTCAGGCTGTTTCGGAGC 120
DB 493 AAGAATGCCCTCTGAAATGAAGTGCCTTTTGTGTACAGGAACAAGATGTTTCCAGTGT 552
QY 121 ACGGTCAAGCAGGTGGAATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
DB 553 GAGTCCGGATGTGAACCTTTGAGGATCCAGCCTCTGCTCTGTGATTCATCAATGATGAG 612
QY 181 GTGAAGAGACACAAAGAGCATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGAC--- 237
DB 613 GTTAAACAAACAGGAGATGATGACAATCTGCTGTCCCAAGATCTTATGATGTT 672
QY 238 CAGCTGAGCGGCTGTTCTGGTGAATGCGCTTACTTCAACGGCCAGTGGAAAAACGCC 297
DB 673 GTGCTCACCAGACTGCTGCTCGTCAACGAGTGTATTTCAAGGGTCTGTGGAAATCAAG 732
QY 298 TTCCAGAGAAAGACTACACCGGCTTTCACAAGTCTGATGGCAGCAGCGTCTCT 357
DB 733 TTCCAAACCGGAGAACACAAAGAACGCACTTTCTGTGGCAGCGACGCGGAAATCTATCAA 792
QY 358 GTGCCCATGATGCTCAGACCAACAGTTCAACTTGGCCAAAGGGGCTGTGGAC--- 417
DB 793 GTGCCAATGCTGCCAGCTCTCCGTGTTCCGGTGTGGTGGTGGTGGTGGTGGTGGTGG 852
QY 418 CATTTACTAGACATCTCTGGAATTCCTACCGGCAACACTCTGAGCATGTTTCATTGCC 477
DB 853 TTATGTTACAATCTTCACTGAACTGCTTACCACGGGGAAGCATCAGCATGCTGATTGCA 912
QY 478 GCCCCTACGAAAGAGGTGCTCTCTCGGCTTCCAGCATCTGAGCATGTTTCAGTCTC 537
DB 913 CTGCCAGCTGAGAGTCCACTCGGCTGTGTCATCATCCACACATCAGCACCAGAAC 972
QY 538 ATCAGCCAGTGA 550
DB 973 ATAGACAGCTGA 985

RESULT 12

5457090-3
; Patent No. 5457090
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,294
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 3
; LENGTH: 2032
5457090-3

Query Match 17.4%; Score 97; DB 9; Length 2032;
Best Local Similarity 49.7%; Pred. No. 2.5e-17;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;
QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
DB 433 AAGGCCATCGTCTCCRAAGAAATAAGACATTTGTGACAGTGGCTAACGCCGTGTTGTT 492
QY 61 CAGGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTACTTTCAGGCTGTTTCGGAGC 120
DB 493 AAGAATGCCCTCTGAAATGAAGTGCCTTTTGTGTACAGGAACAAGATGTTTCCAGTGT 552
QY 121 ACGGTCAAGCAGGTGGAATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
DB 553 GAGTCCGGATGTGAACCTTTGAGGATCCAGCCTCTGCTCTGTGATTCATCAATGATGAG 612

QY 181 GTGAAGAGACACAAAGAGCATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGAC--- 237
DB 613 GTTAAACAAACAGGAGATGATGACAATCTGCTGTCCCAAGATCTTATGATGTT 672
QY 238 CAGCTGAGCGGCTGTTCTGGTGAATGCGCTTACTTCAACGGCCAGTGGAAAAACGCC 297
DB 673 GTGCTCACCAGACTGCTGCTCGTCAACGAGTGTATTTCAAGGGTCTGTGGAAATCAAG 732
QY 298 TTCCAGAGAAAGACTACACCGGCTTTCACAAGTCTGATGGCAGCAGCGTCTCT 357
DB 733 TTCCAAACCGGAGAACACAAAGAACGCACTTTCTGTGGCAGCGACGCGGAAATCTATCAA 792
QY 358 GTGCCCATGATGCTCAGACCAACAGTTCAACTTGGCCAAAGGGGCTGTGGAC--- 417
DB 793 GTGCCAATGCTGCCAGCTCTCCGTGTTCCGGTGTGGTGGTGGTGGTGGTGGTGGTGG 852
QY 418 CATTTACTAGACATCTCTGGAATTCCTACCGGCAACACTCTGAGCATGTTTCATTGCC 477
DB 853 TTATGTTACAATCTTCACTGAACTGCTTACCACGGGGAAGCATCAGCATGCTGATTGCA 912
QY 478 GCCCCTACGAAAGAGGTGCTCTCTCGGCTTCCAGCATCTGAGCATGTTTCAGTCTC 537
DB 913 CTGCCAGCTGAGAGTCCACTCGGCTGTGTCATCATCCACACATCAGCACCAGAAC 972
QY 538 ATCAGCCAGTGA 550
DB 973 ATAGACAGCTGA 985

RESULT 13

US-08-948-997-1
; Sequence 1, Application US/08948997
; Patent No. 608020
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG
; APPLICANT: COLEMAN, TIM
; APPLICANT: LAWRENCE, DANIEL
; TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
; TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,997
; FILING DATE: Oct-10-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. ANDERS BROOKES
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF336
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 89..1318

Qy	261	GAATGCCCTCTACTTCAACGGCCAGTGGAAAAAGCCCTTCCACAGAGAAAGCACTCACCA	320
Db	631	TAATGCTGTCTATTTCAGGGGAAGTGGAGTCGAGTTTAGGCTGAAAATACTAGAAC	690
Qy	321	CCGCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTGCCCATGATGGCTCAGACCAA	380
Db	691	CTTTTCTTTCACTAAAGATGATGAAAGTGAAGTCCAAATTCCAATGATGATCAGCAAGG	750
Qy	381	CAAGTTCAACTACACTGAGTTT	402
Db	751	AGAAATTTTATATGGGAATTT	772

Search completed: March 10, 2006, 01:05:59
Job time : 142.5 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	480.8	86.5		2970	6	US-10-368-995-1	Sequence 1, Appli
2	456.4	82.1		2899	8	US-10-741-600-91	Sequence 91, Appl
3	456.4	82.1		3320	8	US-10-741-600-92	Sequence 92, Appl
4	455.2	81.9		1209	6	US-10-128-706-17	Sequence 17, Appl
5	455.2	81.9		1209	9	US-10-512-496-17	Sequence 17, Appl
6	455.2	81.9		1962	6	US-10-368-995-5	Sequence 5, Appli
7	455.2	81.9		2177	9	US-10-852-335A-45	Sequence 45, Appl
8	455.2	81.9		2660	3	US-09-814-353-20146	Sequence 20146, A
9	455.2	81.9		2870	5	US-10-060-036-131	Sequence 131, App
10	455.2	81.9		2876	6	US-10-128-706-5	Sequence 5, Appli
11	455.2	81.9		2876	6	US-10-170-385-236	Sequence 236, App
12	455.2	81.9		2876	6	US-10-259-609-1	Sequence 1, Appli
13	455.2	81.9		2876	6	US-10-259-609-10	Sequence 10, Appl
14	455.2	81.9		2876	6	US-10-368-995-3	Sequence 3, Appli
15	455.2	81.9		2876	7	US-10-197-258-1	Sequence 1, Appli
16	455.2	81.9		2876	7	US-10-231-956A-419	Sequence 419, App
17	455.2	81.9		2876	7	US-10-641-643-1187	Sequence 1187, App
18	455.2	81.9		2876	9	US-10-956-157-442	Sequence 442, App
19	455.2	81.9		2876	9	US-10-513-496-5	Sequence 5, Appli
20	455.2	81.9		2876	9	US-10-508-406-1	Sequence 1, Appli
21	455.2	81.9		2876	9	US-10-631-467-399	Sequence 399, App
22	455.2	81.9		2937	8	US-10-775-169-229	Sequence 229, App
23	455.2	81.9		3171	6	US-10-240-965-160	Sequence 160, App

Db 668 CTGACAGCGCTGGTCTGGTAAATGCGCTCTACTTCAACGGCCAGTGAAGATGCGCTTC 727
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGATGGCAGCACGCTCTCTGTG 360
Db 728 CCAGAGTCAAAACACCACACCGCTCTTCCCAAGTCCGATGGCAGCACCATCTCTGTG 787
QY 361 CCCATGATGGCTCAGACCAACCAAGTTCAAATCACTAGTTTCCACCCCGCAGCGCCAT 420
Db 788 CCCATGATGGCTCAGACCAACCAAGTTCAAATCACTAGTTTACCAACCCCGCAGCGCT 847
QY 421 TACTAGCACATCTGGAATGGCTTACCAACCGCAACATCTCTGAGCATGTTCAATTCGCGC 480
Db 848 TACTAGCACATCTGGAATGGCTTACCAACCGCAACATCTCTGAGCATGTTCAATTCGCGC 907
QY 481 CCTACGAAAAAGAGTGCTCTCTCCGCGCTCACAGCATCTCTGAGCATCTGAGCTCATC 540
Db 908 CCTATGAGAGAGTGCGCTCTCTGCGCTCACAGCATCTCTGAGCATCTGAGCTCATC 967
QY 541 AGCCAGTGAAGGGA 556
Db 968 AGCCAGTGAAGGGA 983

RESULT 2

US-10-741-600-91
; Sequence 91, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 2899
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-91

Query Match 82.1%; Score 456.4; DB 8; Length 2899;
Best Local Similarity 88.1%; Pred. No. 8.3e-136;
Matches 490; Conservative 5; Mismatches 61; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 60
Db 589 AAGGAGCTCAYGGGCGCATGGAACAAAGAYGAGATCAGCACACAGCGCATCTTCGTG 648
QY 61 CAGCGGATCTGAAGTGGTCCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCCGGACC 120
Db 649 CAGCGGATCTGAAGTGGTCCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCCGGACC 708
QY 121 ACGGTCAGCAGGTGGATTTTTCAGAGATGAGACGAGCCAGGTTTCATCAATGACTGG 180
Db 709 ACGGTCAGCAGGTGGATTTTTCAGAGATGAGACGAGCCAGATTCATCAATGACTGG 768
QY 181 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAGGCGCTGTGGACCG 240
Db 769 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAGGCGCTGTGGACCG 828
QY 241 CTGACGCGCTGGTCTGTAATGCCCTCTACTTCAACGGCCAGTGAAGAACCGCTTC 300
Db 829 CTGACGCGCTGGTCTGTAATGCCCTCTACTTCAACGGCCAGTGAAGAACCGCTTC 888
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 709 ACGGTCAGCAGGTGGATTTTTCAGAGATGAGACGAGCCAGATTCATCAATGACTGG 768
QY 181 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAGGCGCTGTGGACCG 240
Db 769 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAGGCGCTGTGGACCG 828
QY 241 CTGACGCGCTGGTCTGTAATGCCCTCTACTTCAACGGCCAGTGAAGAACCGCTTC 300
Db 829 CTGACGCGCTGGTCTGTAATGCCCTCTACTTCAACGGCCAGTGAAGAACCGCTTC 888
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGATGGCAGCACCGCTCTGTG 360
Db 889 CCGGACTCCAGCACCCACCGCTCTTCCCAATGAGTGGCAGCATCTCTCTGTG 948
QY 361 CCCATGATGGCTCAGACCAACCAAGTTCAAATCACTAGTTTCCACCCCGCAGCGCCAT 420

Db 949 CCCATGATGGCTCAGACCAACCAAGTTCAAATCACTAGTTTCCACACCGCCGATGGCCAT 1008
QY 421 TACTAGCACATCTGGAATGGCTTACCAACCGCAACATCTCTGAGCATGTTCAATTCGCGC 480
Db 1009 TACTAGCACATCTGGAATGGCTTACCAACCGGGACAMCCTCAGCATGTTCAATTCGCGC 1068
QY 481 CCTACGAAAAAGAGTGCTCTCTCCGCGCTCACAGCATCTCTGAGCTCATC 540
Db 1069 CCTATGAGAGAGTGCGCTCTCTGCGCTCACAGCATCTCTGAGTGGCCAGCTCATC 1128
QY 541 AGCCAGTGAAGGGA 556
Db 1129 AGCCAGTGAAGGGA 1144

RESULT 3

US-10-741-600-92
; Sequence 92, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-92

Query Match 82.1%; Score 456.4; DB 8; Length 3320;
Best Local Similarity 88.1%; Pred. No. 8.7e-136;
Matches 490; Conservative 5; Mismatches 61; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 60
Db 589 AAGGAGCTCAYGGGCGCATGGAACAAAGAYGAGATCAGCACACAGCGCATCTTCGTG 648
QY 61 CAGCGGATCTGAAGTGGTCCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCCGGACC 120
Db 649 CAGCGGATCTGAAGTGGTCCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCCGGACC 708
QY 121 ACGGTCAGCAGGTGGATTTTTCAGAGATGAGACGAGCCAGGTTTCATCAATGACTGG 180
Db 709 ACGGTCAGCAGGTGGATTTTTCAGAGATGAGACGAGCCAGATTCATCAATGACTGG 768
QY 181 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAGGCGCTGTGGACCG 240
Db 769 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAGGCGCTGTGGACCG 828
QY 241 CTGACGCGCTGGTCTGTAATGCCCTCTACTTCAACGGCCAGTGAAGAACCGCTTC 300
Db 829 CTGACGCGCTGGTCTGTAATGCCCTCTACTTCAACGGCCAGTGAAGAACCGCTTC 888
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 889 CCGGACTCCAGCACCCACCGCTCTTCCCAATGAGTGGCAGCATCTCTCTGTG 948
QY 361 CCCATGATGGCTCAGACCAACCAAGTTCAAATCACTAGTTTCCACCCCGCAGCGCCAT 420
Db 949 CCCATGATGGCTCAGACCAACCAAGTTCAAATCACTAGTTTCCACCCCGCAGCGCCAT 1008
QY 421 TACTAGCACATCTGGAATGGCTTACCAACCGCAACATCTCTGAGCATGTTCAATTCGCGC 480
Db 1009 TACTAGCACATCTGGAATGGCTTACCAACCGGGACAMCCTCAGCATGTTCAATTCGCGC 1068
QY 481 CCTACGAAAAAGAGTGCTCTCTCAGCGCTCACAGCATCTCTGAGCGCTCAGCTCATC 540
Db 1069 CCTATGAAAAAGAGTGCTCTCTCTGCGCTCACCAACATTCAGTGGCCAGCTCATC 1128

```

Qy      541  AGCCAGTGGAAAGGGA  556
      ||||| ||||| |||||
Db      1129 AGCCACTGGAAAGGCA  1144

RESULT 4
US-10-128-706-17
; Sequence 17, Application US/10128706
; Publication No. US20030199463A1
; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
; FILE REFERENCE: 0575/66601
; CURRENT APPLICATION NUMBER: US/10/128, 706
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-128-706-17

```

Query Match	81.9%	Score 455.2	DB 6	Length 1209
Best Local Similarity	88.7%	Pred. No. 1.4e-135		
Matches 493	Conservative 0	Mismatches 63	Indels 0	Gaps 0
Qy	1	AAGGAGCTCATGGGCGCTGGAA	CAAAAGATGAGATCAGCAGCGCGATGCCATCTTCGTG	60
Db	307	AAGGAGCTCATGGGCGCATGGAA	CAAGATGAGATCAGCAGCGCGATCTTCGTG	366
Qy	61	CAGCGGATCTGAAGCTGGTCCAGGGTTT	TTCATGCCCTACTTCTTCAGCGCTTCCCGGACC	120
Db	367	CAGCGGATCTGAAGCTGGTCCAGGGCTT	CATGCCCACTTCTTCAGCGCTTCCCGGACC	426
Qy	121	ACGGTCAAGCAGGTGGATTTTTCAGAGAT	GGACAGAGCGAGGTTTCATCATCAATGACTGG	180
Db	427	ACGGTCAAGCAAGTGGACTTTTTCAGAGGT	GGAGAGGCGAGATTTCATCAATGACTGG	486
Qy	181	GTGAAGAGACACACAAAAGGCGATGATCA	ATGACTTACTTGGCCAAAGGGCTGTGCACCAAG	240
Db	487	GTGAAGACACACAAAAGGTATGATCAGCA	ACTTGTCTGGAAAGAGCGGTGGAACCAAG	546
Qy	241	CTGACGGCGCTGGTCTTGTTGTAATGCG	CCCTCTACTTCAACCGGCCAGTGGAAACCGCC	300
Db	547	CTGACAGCGGTGGTGGTGAATGCGCCT	CTACTTCAACGGCCAGTGGAAAGACTCCCTTC	606
Qy	301	CCAGAGAAAAGCACTCACACCGGCTCTT	CCACAAAGTCTGATGGCAGCACCGTCTCTGTG	360
Db	607	CCGACTCCAGCACCCACCGCGGCTCTT	CCACAAATCAGACGGCAGCACTGTCTCTGTG	666
Qy	361	CCCATGATGCTCAGACCAACAAGTTCAAC	TACACTGAGTGTTCACGCCCGCAGCGGCAT	420
Db	667	CCCATGATGCTCAGACCAACAAGTTCAAC	TATACTGAGTGTTCACCGCGATGGCCAT	726
Qy	421	TACTACGACATCTGGAAATTTGCCCTAC	CAGGCAACTCTGAGCACTGTTCAATTCGCGCC	480
Db	727	TACTACGACATCTGGAAATCTGCCCTAC	CAGGGAACCCCTCAGCATGTTCAATTCGTGCC	786
Qy	481	CCCTACGAAAAAGAGTGGCTCTCTCGGC	CCCTCACCAGCACTTCGAGCGCTCAGCTCATC	540
Db	787	CCCTATGAAAAAGAGTGGCTCTCTCTGC	CCCTCACCACAAATTCGAGTGCACGCTCATC	846
Qy	541	AGCCAGTGGAAAGGGA	556	
Db	847	AGCCACTGGAAAGGCA	862	

RESULT 5
US-10-512-496-17
; Sequence 17, Application US/10512496
; Publication No. US20050148527A1

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; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
; FILE REFERENCE: 0575/66601-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/512,496
; CURRENT FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-512-496-17

```

Query Match	81.9%;	Score 455.2;	DB 9;	Length 1209;
Best Local Similarity	88.7%;	Pred. No. 1.4e-135;		
Matches 493;	Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;
Qy	1	AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG	60	
Db	307	AAGGAGCTCATGGGCGCATGGAACAGATGAGATCAGCACAGACGCGATCTTCGTG	366	
Qy	61	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGCGTGTTCGCGACC	120	
Db	367	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGCGTGTTCGCGAGC	426	
Qy	121	ACGGTCAGCAGGTGGATTTTTCAGAGATGGACAGAGCGAGGTTTCATCATCAATGACTGG	180	
Db	427	ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG	486	
Qy	181	GTGAAGAGACACACAAAAGGCATGATCAATGACTTTACTTGGCCAAAGGGCTGTGGACCAG	240	
Db	487	GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGGCCGTGGACCAG	546	
Qy	241	CTGACGGGCTGTGTTCTGGTAATGCCCTCTACTTCAACCGGCCAGTGGAAAAACGCCCTTC	300	
Db	547	CTGACACGGCTGTGTTGGTAATGCCCTCTACTTCAACCGGCCAGTGGAAAGTCCCTTC	606	
Qy	301	CCAGAGAAAGCACTCACACACCGCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTCTG	360	
Db	607	CCGACTCAGCACACACCGCGCTCTTCCACAATCAGACGGCAGCACTGTCTCTCTG	666	
Qy	361	CCCATGATGCTCAGACCAACAAGTTTCAACTACACTGAGTTTTCACCCCGGAGGGCCAT	420	
Db	667	CCCATGATGCTCAGACCAACAAGTTTCAACTATACTGAGTTTCAACCGCGGATGGCCAT	726	
Qy	421	TACTACGACATCCTGGAAATGCCCTACCAAGGCAACACTCTGAGCATGTTCAATTCGCGCC	480	
Db	727	TACTACGACATCCTGGAAATGCCCTACCAAGGAGACAACCTTCAGCATGTTTCAATTCGTC	786	
Qy	481	CCCTACGAAAAAGAGTGCCTCTCTCGGCCCTCACACGACTTCTGGACGCTCAGCTCATC	540	
Db	787	CCTTATGAAAAAGAGTGCCTCTCTCTGCCCTCACCAACATTCGTAGTGCCAGTCTCATC	846	
Qy	541	AGCCAGTGGAAAGGGA	556	
Db	847	AGCCACTGGAAAGGCA	862	

RESULT 6
US-10-368-985-5
; Sequence 5, Application US/10368995
; Publication NO. US20030217371A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Eren, Mesut
; APPLICANT: Declerck, Paul J.
; TITLE OF INVENTION: THERAPEUTIC MET
; TITLE OF INVENTION: ANIMAL
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16

;; PRIOR FILING DATE: 2000-07-25
;; PRIOR APPLICATION NUMBER: US 60/257,672
;; PRIOR FILING DATE: 2000-12-21
;; NUMBER OF SEQ ID NOS: 22037
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 20146
;; LENGTH: 2660
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-814-353-20146

Query Match 81.9%; Score 455.2; DB 3; Length 2660;
Best Local Similarity 88.7%; Pred. No. 1.9e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGAGCTCATGGGCGCGTGGAGCAAAAGATGAGATCAGACGCGCGGATGCAATCTTCTGCGT 60
Db 452 AAGAGCTCATGGGCGCGTGGAGCAAAAGATGAGATCAGACGCGCGGATGCAATCTTCTGCGT 511

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTCAAGCTGTTTCCGGACC 120
Db 512 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTCAAGCTGTTTCCGGACC 571

QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGAGCCAGGTTTCATCATCAATGACTGG 180
Db 572 ACGGTCAAGCAGTGGATTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 631

QY 181 GTGAAGAGACACACAAAGGATGATCAATGACTTCTTGGCCAAAGGGGCTGTGGACCAG 240
Db 632 GTGAAGAGACACACAAAGGATGATCAGCAACTTGTCTGGAAAGAGCGGTGGACCAG 691

QY 241 CTGACGCGCTGGTCTGGTGAATGCCCTTCTTCAAGCGCCAGTGGAAAACGCCCTTC 300
Db 692 CTGACGCGCTGGTCTGGTGAATGCCCTTCTTCAAGCGCCAGTGGAAAACGCCCTTC 751

QY 301 CCAGAGAAAAGCACTACACCGCTCTTCCACAAAGTCTCATGCGACGCGTCTGTG 360
Db 752 CCGACTCCAGACCCACCGCGCTCTTCCACAAATCAGACGCGACATGCTCTGTG 811

QY 361 CCCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCCCGACGCGCAT 420
Db 812 CCCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCGCGCATGCGCAT 871

QY 421 TACTAGACATCTGGAATTCCTACCGGCAACAATCTGAGCAATGTTTCATGTCGCC 480
Db 872 TACTAGACATCTGGAATTCCTACCGGCAACAATCTGAGCAATGTTTCATGTCGCC 931

QY 481 CCTTACGAAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTGGACGCTCAGCTCATC 540
Db 932 CCTTATGAAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTGGACGCTCAGCTCATC 591

QY 541 AGCCAGTGGAAAGGGA 556
Db 992 AGCCACTGGAAAGGCA 1007

RESULT 9
US-10-060-036-131
;; Sequence 131, Application US/10060036
;; Publication No. US20030073144A1
;; GENERAL INFORMATION:
;; APPLICANT: Benson, Darin R.
;; APPLICANT: Kalos, Michael D.
;; APPLICANT: Lodes, Michael J.
;; APPLICANT: Persing, David H.
;; APPLICANT: Hepler, William T.
;; APPLICANT: Jiang, Yuqiu
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121-566
;; CURRENT APPLICATION NUMBER: US/10/060,036
;; CURRENT FILING DATE: 2002-01-30
;; NUMBER OF SEQ ID NOS: 4560

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 131
;; LENGTH: 2870
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-036-131

Query Match 81.9%; Score 455.2; DB 5; Length 2870;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGAGCTCATGGGCGCGTGGAGCAAAAGATGAGATCAGACGCGCGGATGCAATCTTCTGCGT 60
Db 376 AAGAGCTCATGGGCGCGTGGAGCAAAAGATGAGATCAGACGCGCGGATGCAATCTTCTGCGT 435

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTCAAGCTGTTTCCGGACC 120
Db 436 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTCAAGCTGTTTCCGGACC 495

QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGAGCCAGGTTTCATCATCAATGACTGG 180
Db 496 ACGGTCAAGCAGTGGATTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 555

QY 181 GTGAAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCAG 240
Db 556 GTGAAGAGACACACAAAGGATGATCAGCAACTTGTCTGGAAAGAGCGGTGGACCAG 615

QY 241 CTGACGCGCTGGTCTGGTGAATGCCCTTCTTCAAGCGCCAGTGGAAAACGCCCTTC 300
Db 616 CTGACGCGCTGGTCTGGTGAATGCCCTTCTTCAAGCGCCAGTGGAAAACGCCCTTC 675

QY 301 CCAGAGAAAAGCACTACACCGCTCTTCCACAAAGTCTCATGCGACGCGTCTGTG 360
Db 676 CCGACTCCAGACCCACCGCGCTCTTCCACAAATCAGACGCGGACATGCTCTGTG 735

QY 361 CCCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCCCGACGCGCAT 420
Db 736 CCCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCGCGCATGCGCAT 795

QY 421 TACTAGACATCTGGAATTCGCCCTACACGCGCAACAATCTGAGCATGTTTCATGTCGCC 480
Db 796 TACTAGACATCTGGAATTCGCCCTACACGCGGCAACAATCTGAGCATGTTTCATGTCGCC 855

QY 481 CCTTACGAAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTGGACGCTCAGCTCATC 540
Db 856 CCTTATGAAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTGGACGCTCAGCTCATC 915

QY 541 AGCCAGTGGAAAGGGA 556
Db 916 AGCCACTGGAAAGGCA 931

RESULT 10
US-10-128-706-5
;; Sequence 5, Application US/10128706
;; Publication No. US20030199463A1
;; GENERAL INFORMATION:
;; APPLICANT: ITESCU, SILVIU
;; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
;; FILE REFERENCE: 0575/66601
;; CURRENT APPLICATION NUMBER: US/10/128,706
;; CURRENT FILING DATE: 2002-04-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 2876
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-10-128-706-5

Query Match 81.9%; Score 455.2; DB 6; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Query Match 81.9%; Score 455.2; DB 6; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

1 AAGGAGCTCATGGGGCCGTGGAAACAAAGATGAGATCAGACCGCGCGGATGCCATCTTCGTG 60
|||
382 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACCGCACAGACCGGATCTTCGTG 441
|||
61 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
|||
442 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 501
|||
121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 180
|||
502 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 561
|||
181 GTGAAGAGACACACAAAAGGATGATCAATGACTTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 240
|||
562 GTGAAGAGACACACAAAAGGATGATCAATGACTTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 621
|||
241 CTGACCGGCTGGTCTGGTGAATGCCCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 300
|||
622 CTGACCGGCTGGTCTGGTGAATGCCCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 681
|||
301 CCAGAGAAAAGCACTCACCACCGCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 360
|||
682 CCGGACTCAGACACCCACCGCGCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 741
|||
361 CCATGATGGCTCAGACCAACAAAGTTTCAACTACTGAGTTTTCACCGCGCGGATGCCAT 420
|||
742 CCATGATGGCTCAGACCAACAAAGTTTCAACTACTGAGTTTTCACCGCGCGGATGCCAT 801
|||
421 TACTAGGATCTGGAATGGCTTACACCGGCAACACTCTGAGCATGTTCAATTCGCGCC 480
|||
802 TACTAGGATCTGGAATGGCTTACACCGGCAACACTCTGAGCATGTTCAATTCGCGCC 861
|||
481 CCTACGAAAAGAGTGCTCTCTCGCGCTTCCAGCATTTCTGAGCATGTTCAATTCGCGCC 540
|||
862 CTTATGAAAAGAGTGCTCTCTCGCGCTTCCAGCATTTCTGAGCATGTTCAATTCGCGCC 921
|||
541 AGCCAGTGGAAAGGGA 556
|||
922 AGCCACTGGAAAGGCA 937
|||

RESULT 11

US-10-170-385-236

; Sequence 236, Application US/10170385

; Publication No. US20030203372A1

; GENERAL INFORMATION:

; APPLICANT: Ward, Neil Raymond

; APPLICANT: Mundy, Christopher Robert

; APPLICANT: Kan, On

; APPLICANT: Harris, Robert Alan

; APPLICANT: White, Jonathan

; APPLICANT: Binley, Katie Mary

; APPLICANT: Rayner, William Nigel

; APPLICANT: Naylor, Stuart

; APPLICANT: Kingsman, Susan Mary

; APPLICANT: Krige, David

; TITLE OF INVENTION: ANALYSIS METHOD

; FILE REFERENCE: 532682000100

; CURRENT APPLICATION NUMBER: US/10/170,385

; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: PCT/GB02/01662

; PRIOR FILING DATE: 2002-04-08

; PRIOR APPLICATION NUMBER: PCT/GB01/05458

; PRIOR FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 549

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 236

; LENGTH: 2876

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-170-385-236

Query Match 81.9%; Score 455.2; DB 6; Length 2876;

Best Local Similarity 88.7%; Pred. No. 2e-135;

Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Query Match 81.9%; Score 455.2; DB 6; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

1 AAGGAGCTCATGGGGCCGTGGAAACAAAGATGAGATCAGACCGCGCGGATGCCATCTTCGTG 60
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382 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACCGCACAGACCGGATCTTCGTG 441
|||
61 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
|||
442 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 501
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121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 180
|||
502 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 561
|||
181 GTGAAGAGACACACAAAAGGATGATCAATGACTTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 240
|||
562 GTGAAGAGACACACAAAAGGATGATCAATGACTTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 621
|||
241 CTGACCGGCTGGTCTGGTGAATGCCCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 300
|||
622 CTGACCGGCTGGTCTGGTGAATGCCCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 681
|||
301 CCAGAGAAAAGCACTCACCACCGCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 360
|||
682 CCGGACTCAGACACCCACCGCGCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 741
|||
361 CCATGATGGCTCAGACCAACAAAGTTTCAACTACTGAGTTTTCACCGCGCGGATGCCAT 420
|||
742 CCATGATGGCTCAGACCAACAAAGTTTCAACTACTGAGTTTTCACCGCGCGGATGCCAT 801
|||
421 TACTAGGATCTGGAATGGCTTACACCGGCAACACTCTGAGCATGTTCAATTCGCGCC 480
|||
802 TACTAGGATCTGGAATGGCTTACACCGGCAACACTCTGAGCATGTTCAATTCGCGCC 861
|||
481 CCTACGAAAAGAGTGCTCTCTCGCGCTTCCAGCATTTCTGAGCATGTTCAATTCGCGCC 540
|||
862 CTTATGAAAAGAGTGCTCTCTCGCGCTTCCAGCATTTCTGAGCATGTTCAATTCGCGCC 921
|||
541 AGCCAGTGGAAAGGGA 556
|||
922 AGCCACTGGAAAGGCA 937
|||

RESULT 12

US-10-259-609-1

; Sequence 1, Application US/10259609

; Publication No. US20030216321A1

; GENERAL INFORMATION:

; APPLICANT: LAWRENCE, Daniel A

; APPLICANT: STEFANSON, Steingrimsur P

; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THE

; FILE REFERENCE: 30523/167

; CURRENT APPLICATION NUMBER: US/10/259,609

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US/09/324,494A

; PRIOR FILING DATE: 1999-06-02

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 2876

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (76)..(1281)

; OTHER INFORMATION:

US-10-259-609-1


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Db 502 |ACGGTCAAGCAAGTGACATTTT|CAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 561
Qy 181 |GTGAAGAGACACACAAAAGGCATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGACCAG 240
Db 562 |GTGAAGAGACACACAAAAGGTATGATCAGCAACTTGTCTTGGAAAGGAGCCGTGGACCAG 621
Qy 241 |CTGACGCGCTGGTTCTGGTGAATGCGCTCTACTTCAACGGGCAGTGGAAAACGCGCTTTC 300
Db 622 |CTGACACGGCTGGTGTGGTGAATGCGCTCTACTTCAACGGGCAGTGGAAAGACTCCCTTC 681
Qy 301 |CCAGAGAAAAGCACTCACACCGCTCTTCCACAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 682 |CCCGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 741
Qy 361 |CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTCCACCCCGACGGCCAT 420
Db 742 |CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTCCACCGCCGATGGCCAT 801
Qy 421 |TACTACGACATCCTGGAATTGCGCTTACCAACGGCAACACTCTGAGCATGTTCAATGCGGCC 480
Db 802 |TACTACGACATCCTGGAATGCGCTTACCAACGGGCACACCTCAGCATGTTCAATGCTGCC 861
Qy 481 |CCCTACGAAAAGAGTGCTCTCTCGGCCCTCACAGCAITTCAGGACGCTCAGCTCATC 540
Db 862 |CCTTATGAAAAGAGTGCTCTCTCGGCCCTCACCAACATTCAGTGTGCCAGCTCATC 921
Qy 541 |AGCCAGTGGAAAGGGA 556
Db 922 |AGCCACTGGAAGGCA 937
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RESULT 15

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US-10-197-258-1
; Sequence 1, Application US/10197258
; Publication No. US20040014190A1
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: GORLATOVA, NATALIA
; APPLICANT: CRANDALL, DAVID L.
; TITLE OF INVENTION: MUTANT PROTEINASE-INHIBITORS AND USES THEREOF
; FILE REFERENCE: 030523-0187
; CURRENT APPLICATION NUMBER: US/10/197,258
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1281)
US-10-197-258-1
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Query Match 81.9%; Score 455.2; DB 7; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGATGATCAGACGGCCGATGCCATCTTCGTG 60
Db 382 AAGGAGCTCATGGGCGCATGGAAACAAAGATGATGATCAGACGGCCGATCTTCGTG 441
Qy 61 CAGCGGATCTGAAGTGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
Db 442 CAGCGGATCTGAAGTGTCCAGGGCTTCATGCCCTACTCTTCAGGCTGTTCGGAGC 501
Qy 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGGACAGAGCCAGGTTCATCATCAATGACTGG 180
Db 502 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 561
Qy 181 GTGAAGAGACACACAAAAGGCATGATCAATGACTTCTTGGCCAAAGGGCTGTGGACCAG 240
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Job time : 676 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Maximum Match 100%
Listing first 45 summaries

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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	455.2	81.9	1209	8	US-10-821-234-729
2	455.2	81.9	2522	12	US-11-094-519A-11
3	455.2	81.9	2876	12	US-11-091-883-114
4	455.2	81.9	2937	8	US-10-775-169-229
5	455.2	81.9	3273	12	US-11-091-883-113
6	420	75.5	2038	12	US-11-136-527-3753
7	394.2	70.9	2438	12	US-11-094-519A-10
8	176.6	31.8	1404	8	US-10-750-185-46781
9	176.6	31.8	1404	8	US-10-750-623-46781
10	157.6	28.3	14302	12	US-11-136-527-3649
11	98.6	17.7	1191	9	US-11-245-147-95
12	98.6	17.7	1197	8	US-10-821-234-636
13	98.6	17.7	2129	12	US-11-186-284-184
14	96.6	17.4	1963	12	US-11-136-527-1947
15	93.2	16.8	1212	9	US-11-245-147-20
16	80.8	14.5	1398	7	US-10-959-322-2
17	74.8	13.5	1559	8	US-10-955-054A-47
18	74.6	13.4	1378	12	US-11-128-061-873
19	74.6	13.4	1378	12	US-11-128-049-873
20	69.4	12.5	1370	9	US-11-048-774-12

21	69.4	12.5	1371	9	US-11-048-774-1	Sequence 1, Appli
22	69	12.4	1736	8	US-10-995-561-409	Sequence 409, App
23	69	12.4	1911	8	US-10-995-561-410	Sequence 410, App
24	68.2	12.3	2081	12	US-11-128-061-1036	Sequence 1036, Ap
25	68.2	12.3	2081	12	US-11-128-049-1036	Sequence 1036, Ap
26	67.8	12.2	1900	8	US-10-775-169-49	Sequence 49, Appl
27	67.8	12.2	1900	12	US-11-091-883-135	Sequence 135, App
28	67.6	12.2	1299	7	US-10-959-322-40	Sequence 40, Appl
29	67.6	12.2	1395	7	US-10-959-309-18	Sequence 18, Appl
30	67.6	12.2	1395	7	US-10-959-322-1	Sequence 1, Appli
31	67.6	12.2	1599	9	US-11-129-861-43	Sequence 43, Appl
32	66.2	11.9	1918	8	US-10-821-234-48	Sequence 48, Appl
33	65.2	11.7	1254	12	US-11-147-047-13	Sequence 13, Appl
34	64.8	11.7	1782	12	US-11-178-134-13	Sequence 13, Appl
35	64.6	11.6	1398	12	US-11-136-527-309	Sequence 309, App
36	64.2	11.5	1400	12	US-11-136-527-6043	Sequence 6043, Ap
37	63.2	11.4	1466	8	US-10-276-233A-14	Sequence 14, Appl
38	63.2	11.4	2480	9	US-11-072-512-1410	Sequence 1410, Ap
39	62.8	11.3	1606	8	US-10-995-561-278	Sequence 278, App
40	62.8	11.3	1655	8	US-10-995-561-277	Sequence 277, App
41	62.8	11.3	2480	8	US-10-995-561-276	Sequence 276, App
42	61.2	11.0	2941	8	US-10-995-561-242	Sequence 242, App
43	61.2	11.0	3035	8	US-10-995-561-238	Sequence 238, App
44	61.2	11.0	3079	8	US-10-995-561-239	Sequence 239, App
45	61.2	11.0	3124	8	US-10-995-561-240	Sequence 240, App

ALIGNMENTS

RESULT 1
US-10-821-234-729
; Sequence 729, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 729
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-729

Query Match	81.9%	Score	455.2	DB	8	Length	1209
Best Local Similarity	88.7%	Pred. No.	1.3e-123				
Matches	493	Conservative	0	Mismatches	63	Indels	0
Gaps	0						
QY	1	AAGGACCTCATGGGCGCGTGGACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTC	60				
Db	307	AGGAGCTCATGGGCGCGTGGACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTC	366				
QY	61	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGGTGTTCGGGACC	120				
Db	367	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGGTGTTCGGGACC	426				
QY	121	ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGCAGCGGTTCATCAATCAATCTGG	180				
Db	427	ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGCAGCGGTTCATCAATCAATCTGG	486				
QY	181	GTCAAGACACACACAAAGGCATGATCACTTACTTGGCCAGGGCTGTGGACCCAG	240				
Db	487	GTCAAGACACACACAAAGGCATGATCACTTACTTGGCCAGGGCTGTGGACCCAG	546				

QY 241 CTGACGGCGCTGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCGCTTC 300
DB 547 CTGACCGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGTATGGCAGCAGCGCTCTCTGTG 360
DB 607 CCGGACTCCAGACCCACCGCGCTCTTCCCAAAATCAGCGCGCACTGTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACACCCCGCAGCGCCAT 420
DB 667 CCCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACCAACCGCGCATGGCCAT 726
QY 421 TACTAGCACTCTGGAATGGCTTACACGGCAACACTCTGAGCATGTTCATGTGCGCC 480
DB 727 TACTAGCACTCTGGAATGGCTTACACGGCAACACTCTGAGCATGTTCATGTGCGCC 786
QY 481 CCTACGAAAAGAGGTGCTCTCTCGGCCCTCACAGCATTTGAGCGCTCAGCTCATC 540
DB 787 CTTTATGAAAAGAGGTGCTCTCTCGGCCCTCACCAACATTTGAGTCCCGCAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
DB 847 AGCCACTGGAAGGCA 862

RESULT 2

US-11-094-519A-11
; Sequence 11, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-11

Query Match 81.9%; Score 455.2; DB 12; Length 2522;
Best Local Similarity 88.7%; Pred. No. 1.6e-123;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
DB 454 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 513
QY 61 CAGCGGATCTCAAGTGTCTCAGGTTTCATGCCCTTCTTCCAGGCTGTTCGGACC 120
DB 514 CAGCGGATCTCAAGTGTCTCAGGTTTCATGCCCTTCTTCCAGGCTGTTCGGAGC 573
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGCGCGATTCATCAATGACTGG 180
DB 574 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGCGCGATTCATCAATGACTGG 633
QY 181 GTGAAGAGACACAAAAGGATGATCAATGACTTCTTCAAGGCGAGTGGAAAGCGCTTC 240
DB 634 GTGAAGAGACACAAAAGGATGATCAATGACTTCTTCAAGGCGAGTGGAAAGCGCTTC 693
QY 241 CTGACGGCGCTGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGCGCTTC 300
DB 694 CTGACGGCGCTGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 753
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTTCACAAAGTCTGATGGCAGCAGCGCTCTGTG 360

DB 754 CCCGACTCCAGCACCCACCGCGCTCTTCCAAAATCAGACGGCAGCACTGTCTGTG 813
QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACACCCCGCAGCGCCAT 420
DB 814 CCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACACCGCGCATGGCCAT 873
QY 421 TACTAGCACTCTGGAATGGCTTACACGGCAACACTCTGAGCATGTTCATGTGCGCC 480
DB 874 TACTAGCACTCTGGAATGGCTTACACGGCAACACTCTGAGCATGTTCATGTGCGCC 933
QY 481 CCTACGAAAAGAGGTGCTCTCTCGGCCCTCACAGCATTTGAGCGCTCAGCTCATC 540
DB 934 CTTTATGAAAAGAGGTGCTCTCTCGGCCCTCACCAACATTTGAGTCCCGCAGCTCATC 993
QY 541 AGCCAGTGGAAAGGGA 556
DB 994 AGCCACTGGAAGGCA 1009

RESULT 3

US-11-091-883-114
; Sequence 114, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; TITLE OF INVENTION: VIABILITY
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 114
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-114

Query Match 81.9%; Score 455.2; DB 12; Length 2876;
Best Local Similarity 88.7%; Pred. No. 1.6e-123;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
DB 382 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 441
QY 61 CAGCGGATCTCAAGTGTCTCAGGTTTCATGCCCTTCTTCCAGGCTGTTCGGACC 120
DB 442 CAGCGGATCTCAAGTGTCTCAGGTTTCATGCCCTTCTTCCAGGCTGTTCGGAGC 501
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGCGCGATTCATCAATGACTGG 180
DB 502 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGCGCGATTCATCAATGACTGG 561
QY 181 GTGAAGAGACACAAAAGGATGATCAATGACTTCTTGGCCAGGCGCTGTGGACAG 240
DB 562 GTGAAGAGACACAAAAGGATGATCAATGACTTCTTGGCCAGGCGCTGTGGACAG 621
QY 241 CTGACGGCGCTGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGCGCTTC 300
DB 622 CTGACAGCGCTGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGCTCCCTTC 681
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTTCACAAAGTCTGATGGCAGCAGCGCTCTGTG 360
DB 682 CCCGACTCCAGCACCCACCGCGCTCTTTCACAAAATCAGACGGCAGCACTGTCTCTGTG 741

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Qy	421	TACTACGACATCCTGGAAATGGCCCTTACCACGCGCAACACTCTGAGCATGTTCAATGGCGGC	480
Db	802	TACTACGACATCCTGGAAATGGCCCTTACCACGCGGACACCCCTCAGCATGTTCAATGGTCGC	861
Qy	481	CCCTACGAAAAAGAGGTGCCTCTCTCCGCCCTCACCAACATTCGAGGCTCAGCTCATC	540
Db	862	CCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCAACAATTCGAGTGCCAGCTCATC	921
Qy	541	AGCCAGTGGAAAGGGA	556
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RESULT 4

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US-10-775-169-229
; Sequence 229, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 229
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-229

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Query Match	81.9%;	Score 455.2;	DB 8;	Length 2937;
Best Local Similarity	88.7%;	Pred. No. 1.6e-123;		
Matches 493;	Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;
QY	1	AAGGAGCTCATGGGCGGTGGAAACAAAGATCAGATCAGCAGCGCGGATGCCATCTTCGTG	60	
Db	250	ARGAGCTCATGGGCCATCGAACAGATCAGATCAGCACAGACCGCATCTTCGTC	309	
QY	61	CAGCGGATCTGAAGCTGTGCCAGGGTTTCATGCCCTACTTCTTCAGCGTGTTCGCGACC	120	
Db	310	CAGCGGATCTGAAGCTGTGCCAGGGTTTCATGCCCTACTTCTTCAGCGTGTTCGCGACC	369	
QY	121	ACGGTCAAGCAGGTGGATTTTTCAGAGATCGACAGAGCCAGGTTTCATCAATCAATGACTGG	180	
Db	370	ACGGTCAAGCAAGTGACTTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG	429	
QY	181	GTGAAGAGACACAAAAGGCATGATCAATGACTTACTTGGCCAAAGGGGTGTGGACCAG	240	
Db	430	GTGAAGACACACAAAAGGTATGATCAGCAACTTGTTCGGAAAGAGCGGTGGACCAG	489	
QY	241	CTGACGCGCTGTCTCTGTGAATGCCCTCTACTTCAACGCCAGTGGAAAACGCCCTTC	300	
Db	490	CTGACACGGTGTGTGTGAATGCCCTCTACTTCAACGCCAGTGGAAAGACTCCCTTC	549	
QY	301	CCAGAGAAAGCACTCACACCGCCCTTTCCACAAGTCTGATGCGACACCGCTCTCTGTG	360	
Db	550	CCCGACTCCAGCACCCACCGCGCCTTTCCACAAATCAGACGCGCAGCTGTCTCTGTG	609	
QY	361	CCCATGATGGCTCAGACACACAGTTTCACTACACTGAGTTTTCCACCCCGACGGCCAT	420	
Db	610	CCCATGATGGCTCAGACACACAGTTTCACTACACTGAGTTTTCCACCCCGACGGCCAT	669	
QY	421	TACTACGACATCTCGAAATTGCCCTACTCAGCGCAACACTCTGAGCATGTTTCAATTCGCGCC	480	

Db	670	TACTACGACATCTCGGAATGCCCTACACGGGACACCCTCAGCATGTTCATTGCTGCC	729
Qy	481	CCCTACGAAAAAGAGTGCCTCTCTCCGCCCTCACCGACATTTCTGGAGCTCAGCTCATC	540
Db	730	CTTTATGAAAAAGAGTGCCTCTCTCTGCCCTCACCAACATTTCTGAGTGCCCGAGCTCATC	789
Qy	541	AGCCAGTGGAAAGGCA	556
Db	790	AGCCACTGGAAAGCA	805

RESULT 5

```

US-11-091-883-113
; Sequence 113, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; TITLE OF INVENTION: VIABILITY
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091.883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 113
; LENGTH: 3273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (23)..(25)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (28)..(28)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (36)..(36)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (38)..(38)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (40)..(40)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1486)..(1486)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1546)..(1546)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1719)..(1719)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1835)..(1835)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:

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LENGTH: 3053
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-3753

Query Match 75.5%; Score 420; DB 12; Length 3053;
Best Local Similarity 84.7%; Pred. No. 3.5e-113;
Matches 471; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
DB 425 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 484

QY 61 CAGCGGATCTGAAGCTGGTCCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 120
DB 485 CAGCGGATCTGAAGCTGGTCCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 544

QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180
DB 545 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 604

QY 181 GTGAGAGACACACAAAGGCGTATCAATGATCTTACTTGGCCAAAGGCGTGTGGACCAG 240
DB 605 GTGAGAGGACACAAAGGCGTATCAATGATCTTACTTGGCCAAAGGCGTGTGGACCAG 664

QY 241 CTGACGCGCTGTCTGTGTAATGCCCTTCTTCAAGCGGCGAGTGGAAAGCGCCCTTC 300
DB 665 CTGACGCGCTGTCTGTGTAATGCCCTTCTTCAAGCGGCGAGTGGAAAGCGCCCTTC 724

QY 301 CCAGAGAAAGCACTCACACCGCTTCTTCCAAAGTCTGTGCGCAGCCGCTCTGTG 360
DB 725 TTAGAGCCAGACCCACAGCGCTGTTCACAGTCTGTGAGTGTGAGCCATCTCGTG 784

QY 361 CCATGATGCTCAGACCAACAAAGTTCACACTACAGTGTTCACCGCCGCGCCAT 420
DB 785 CCATGATGCTCAGACCAACAAAGTTCACACTACAGTGTTCACCGCCGCGCCAT 844

QY 421 TACTAGCATCTGGAATGCCCTTACCGGCAACACTCTGAGCATGTTTCATTCGCGC 480
DB 845 GAGTACGATCTGGAATGCCCTTACCGGCAACACTCTGAGCATGTTTCATTCGCGC 904

QY 481 CCTTACGAAAGAGGTCTCTCTCGGCTCACCAGCATTCGTGACGCTCAGCTCATC 540
DB 905 CCTTACGAAAGAGGTCTCTCTCGGCTCACCAGCATTCGTGACGCTCAGCTCATC 964

QY 541 AGCCAGTGGAAAGGA 556
DB 965 AGCAATGGAAGCA 980

RESULT 7
US-11-094-519A-10
; Sequence 10, Application US/11094519A
; Publication No. US2005028180A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-10

Query Match 70.9%; Score 394.2; DB 12; Length 2438;
Best Local Similarity 88.9%; Pred. No. 1.2e-105;
Matches 426; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
DB 454 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 513

QY 61 CAGCGGATCTGAAGCTGGTCCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 120
DB 514 CAGCGGATCTGAAGCTGGTCCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 573

QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180
DB 574 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 633

QY 181 GTGAGAGACACACAAAGGCGTATCAATGATCTTACTTGGCCAAAGGCGTGTGGACCAG 240
DB 634 GTGAGAGACACACAAAGGCGTATCAATGATCTTACTTGGCCAAAGGCGTGTGGACCAG 693

QY 241 CTGACGCGCTGTCTGTGTAATGCCCTTCTTCAAGCGGCGAGTGGAAAGCGCCCTTC 300
DB 694 CTGACGCGCTGTCTGTGTAATGCCCTTCTTCAAGCGGCGAGTGGAAAGCGCCCTTC 753

QY 301 CCAGAGAAAGCACTCACACCGCTTCTTCCAAAGTCTGTGCGCAGCCGCTCTGTG 360
DB 754 CCAGAGAAAGCACTCACACCGCTTCTTCCAAAGTCTGTGCGCAGCCGCTCTGTG 813

QY 361 CCATGATGCTCAGACCAACAAAGTTCACACTACAGTGTTCACCGCCGCGCCAT 420
DB 814 CCATGATGCTCAGACCAACAAAGTTCACACTACAGTGTTCACCGCCGCGCCAT 873

QY 421 TACTAGCATCTGGAATGCCCTTACCGGCAACACTCTGAGCATGTTTCATTCGCGC 479
DB 874 TACTAGCATCTGGAATGCCCTTACCGGCAACACTCTGAGCATGTTTCATTCGCGC 932

RESULT 8
US-10-750-185-46781
; Sequence 46781, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46781
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Bovine 19866880662738
US-10-750-185-46781

Query Match 31.8%; Score 176.6; DB 8; Length 1404;
Best Local Similarity 90.8%; Pred. No. 8e-42;
Matches 188; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 194 CAAAGGCGATGATCAATGATCTTACTTGGCCAAAGGCGTGTGACCGAGCTGACGCGCTGG 253
DB 958 CCATAGGCGATGATGAGCGACTTACTTGGTGAAGGCGTGTGACCGAGCTGACCGCTGG 1017

QY 254 TTCTGTGAATGCCCTTCTTCAAGCGGCGAGTGGAAAGCGCCCTTCCAGAGAAAGCA 313

Db 1018 TCTGGTAAATGCCCTCTACTTCAACGGCCAGTGAAGATGCCCTTCCAGAGTCAAAACA 1077
QY 314 CTCAACACCGCCTCTTCCCAAGTCTGATGGCAGCACCGTCTCTGTGCGCCATGATGGCTC 373
Db 1078 CCCACACCGCCTCTTCCCAAGTCCGATGGCAGCACCATCTCTGTGCCCATGATGGCTC 1137

QY 374 AGACCAACAAGTCAACTACACTGAGT 400
Db 1138 AGACCAACAAGTCAACTACACTGAGT 1164

RESULT 9

US-10-750-623-46781
; Sequence 46781, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46781
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Bovine 19866880662738
US-10-750-623-46781

Query Match 31.8%; Score 176.6; DB 8; Length 1404;
Best Local Similarity 90.8%; Pred. No. 8e-42;
Matches 188; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 194 CAAAGGCATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACAGCTGACGCGCCTGG 253
Db 958 CCAAGGCATGATCAGCGACTTACTTGGTGAAGGGGCTGTGGACAGCTGACAGCCTGG 1017
QY 254 TCTGGTGAATGCCCTCTACTTCAACGGCCAGTGAAGAGCCCTTCCAGAGAAAGCA 313
Db 1018 TCTGGTAAATGCCCTCTACTTCAACGGCCAGTGAAGATGCCCTTCCAGAGTCAAAACA 1077
QY 314 CTCAACACCGCCTCTTCCCAAGTCTGATGGCAGCACCGTCTCTGTGCCCATGATGGCTC 373
Db 1078 CCCACACCGCCTCTTCCCAAGTCCGATGGCAGCACCATCTCTGTGCCCATGATGGCTC 1137
QY 374 AGACCAACAAGTCAACTACACTGAGT 400
Db 1138 AGACCAACAAGTCAACTACACTGAGT 1164

RESULT 10

US-11-136-527-3649
; Sequence 3649, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3649
; LENGTH: 14302
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3649

Query Match 28.3%; Score 157.6; DB 12; Length 14302;
Best Local Similarity 85.8%; Pred. No. 5.7e-36;
Matches 175; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
Db 5159 AAGGAGCTCATGGGGCTCATGGAAACAAGATGAGATCAGTACTGCGGACGCCATCTTTGTC 5218
QY 61 CAGGGGATCTGAAGCTGTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGGACC 120
Db 5219 CAGGGGACCTAGAGCTGGTCCAGGGCTTCATGCCCTACTTCTTCAGGCTGTTCGGGACC 5278
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGCCAGGTTTCATCAATGACTGG 180
Db 5279 ACGGTGAAGCAGGTGGACTTCTCAGAGGTGGAAGAGCCAGATTTCATCAACGACTGG 5338
QY 181 GTGAAGACACACAAAGGCATG 204
Db 5339 GTGGAGAGGCACACCAAGGTAGG 5362

RESULT 11

US-11-245-147-95
; Sequence 95, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 95
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-95

Query Match 17.7%; Score 98.6; DB 9; Length 1191;
Best Local Similarity 49.9%; Pred. No. 6e-19;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

QY 1 AAGGAGCTCATGGGGCCGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
Db 289 AAGGCTATCGTCTCCAAGAAATAAAGACATTGTGACAGTGGCTTAACGCCGTGTTGTT 348
QY 61 CAGGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGGACC 120
Db 349 AAGATGCTCTGAATTAAGTGCCTTTTGTACAGGAACAAGATGTGTTCAGTGT 408
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGCCAGGTTTCATCAATGACTGG 180
Db 409 GAGGTCCGGAATGTCAACTTTGAGGATCCAGCCTCTGCTGTGATTCATCAATGACTGG 468

181 GTGAGAGACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA- 239
469 GTTAAACAAACAGGAGATGATGACAACTGCTGTGCCAGATCTTATGATGGT 528
240 --GCTAGCGCCCTGTGTTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAAGCGCCC 297
529 GTGCTACACAGACTGTGCTCGTCAAGCGAGTGTATTTCAAGGGTCTGTGGAAATCACGG 588
298 TTCCAGAGAAAAGCACTCACCGGCTCTTCCAAAGTCTGATGGCAGCAGCGTCTCT 357
589 TTCCAAACCCGAGAACACAAAAGACGCACTTGTGGCAGCCGCGGAAATCCTATCAA 648
358 GTGCCATGATGGCTCAGACCAACAAAGTTCACACTGAGTTTCCACCCCGGAGGC 417
649 GTGCCATGCTGGCCAGCTCTCGGTTCGGGTGCGAGTGGTGCACAGTGGCCCAATGAT 708
418 CATTACTACGATCTCGGAAATTTGCCCTACCGGCAACACTCTGAGCATGTTCAATTGCC 477
709 TTATGGTACAACTTCAATGAACTGCCCTACCGGGAAGCATCAGCATGCTGATTGCA 768
478 GCCCCTACGAAAAGAGGTGCTCTCTCGCCCTCACGAGCATTTGGACGCTCAGCTC 537
769 CTGCCAGTACGAGCTCCACTCGCTGTCTGCCATCATCCACACATCAGCACCAGACC 828
538 ATCAGCCAGTGA 550
829 ATAGACAGCTGA 841

RESULT 12
US-10-821-234-636
; Sequence 636, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhang
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 636
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-636

Query Match 17.7%; Score 98.6; DB 8; Length 1197;
Best Local Similarity 49.9%; Pred. No. 6e-19;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

QY 1 AAGAGCTCATGGGCGGTGGAAAGATGAGATCAGCAGCGCCGATGCCATCTTCGTG 60
DB 289 AAGGCCATCGTCTCCAAAGAATAAAGACATTTGTGACAGTGGCTAACGCCGTGTTGTT 348
QY 61 CAGCGGATCTGAGCTGGTCCAGGTTTCATGCCCTACTCTTCAAGGCTGTTCGGACC 120
DB 349 AAGAATGCTCTGAAATTTGAAGTGGCTTTGTGTACAAAGGAACAAAGATGTTCAGTGT 408
QY 121 ACAGTCAACAGCTGATTTTTCAGAGATGGACAGAGCCAGGTTCATCATCAATGACTGG 180
DB 409 GAGTCCGGAATGTGAATTTGAGGATCCAGCTCTGCTCTGATTTCCATCAATGATGAG 468
QY 181 GTGAAGAGACACAAAAGGCAATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA- 239
DB 469 GTTAAACAAACAGGAGATGATGACAACTGCTGTGCCAGATCTTATGATGGT 528
QY 240 --GCTAGCGCCCTGTGTTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAAGCGCCC 297

529 GTGCTCACCAGACTGTCTCTGTCACAGCAGTGTATTTCAAGGGTCTGTGGAAATCACGG 588
298 TTCCAGAGAAAAGCACTCACCGCCTCTTCCAAAGTCTCATGGCAGCAGCGTCTCT 357
589 TTCCAAACCCGAGAACACAAAAGACGCACTTTCGTGGCAGCCGCGGAAATCCTATCAA 648
358 GTGCCATGATGGCTCAGACCAACAAAGTTCACACTGAGTTTTCACCCCGGAGGC 417
649 GTGCCATGCTGGCCAGCTCTCGGTTCGGGTGCGAGTGGTGCACAAAGTGGCCCAATGAT 708
418 CATTACTACGATCTCGGAAATTTGCCCTACCGGCAACACTCTGAGCATGTTCAATTGCC 477
709 TTATGGTACAACTTCAATGAACTGCCCTACCGGGAAGCATCAGCATGCTGATTGCA 768
478 GCCCCTACGAAAAGAGGTGCTCTCTCGCCCTCACGAGCATTTGGACGCTCAGCTC 537
769 CTGCCAGTACGAGCTCCACTCGCTGTCTGCCATCATCCACACATCAGCACCAGACC 828
538 ATCAGCCAGTGA 550
829 ATAGACAGCTGA 841

RESULT 13
US-11-186-284-184
; Sequence 184, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhang
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 2129
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210)...(1406)
US-11-186-284-184

Query Match 17.7%; Score 98.6; DB 12; Length 2129;
Best Local Similarity 49.9%; Pred. No. 7.1e-19;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

QY 1 AAGAGCTCATGGGCGGTGGAAAGATGAGATCAGCAGCGCCGATGCCATCTTCGTG 60
DB 498 AAGGCCATCGTCTCCAAAGAATAAAGACATTTGTGACAGTGGCTAACGCCGTGTTGTT 557
QY 61 CAGCGGATCTGAGCTGGTCCAGGTTTTCATGCCCTACTCTTTCAGGCTGTTCGGACC 120
DB 558 AAGAATGCTCTGAAATTTGAAGTGGCTTTTGTGTACAAAGGAACAAAGATGTGTTCAGTGT 617

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:05 ; Search time 5640 Seconds
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_hic:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_est7:*
- 9: gb_gss1:*
- 10: gb_gss2:*
- 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	455.2	81.9	813	BG829624	BG829624 602763976
3	455.2	81.9	932	BE905905	BE905905 601495570
4	455.2	81.9	1027	BX396693	BX396693 BX396693
5	455.2	81.9	1168	AY402982	AY402982 Pan trogl
6	455.2	81.9	1209	AY402981	AY402981 Homo sapi
7	455.2	81.9	1474	CRG14829	CRG14829 full-length
8	454.8	81.8	1019	BX379573	BX379573 BX379573
9	454.8	81.8	1085	BX335507	BX335507 BX335507
10	454.4	81.7	1028	BX425037	BX425037 BX425037
11	453.6	81.6	1116	BX446279	BX446279 BX446279
12	452.6	81.4	817	BI870529	BI870529 603394394
13	450	80.9	894	CA489543	CA489543 AGENCOURT
14	450	80.9	1029	BX382561	BX382561 BX382561
15	444.4	79.9	971	BX417006	BX417006 BX417006
16	444.4	79.9	1017	BX439383	BX439383 BX439383
17	444.4	79.9	1093	BX356157	BX356157 BX356157
18	444.2	79.9	749	BI224426	BI224426 602940982
19	444.2	79.9	829	CD609138	CD609138 56081741J
20	444.2	79.9	1010	BX340248	BX340248 BX340248
21	444.2	79.9	1124	BX378424	BX378424 BX378424
22	443.8	79.8	832	BX379609	BX379609 BX379609

c

Query Match 81.9%; Score 455.2; DB 7; Length 659;

Best Local Similarity 88.7%; Pred. No. 4.3e-115;

Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

23	443.6	79.8	996	5	BX377975	BX377975
24	443.4	79.7	694	1	AUI39624	AUI39624
25	443.2	79.7	616	7	CN485218	CN485218
26	442.6	79.6	975	1	AL545394	AL545394
27	441.4	79.4	581	3	BP237212	BP237212
28	441	79.3	931	5	BUS40881	BUS40881
29	439.8	79.1	853	5	BX344504	BX344504
30	439.2	79.0	1019	1	AL550303	AL550303
31	437.2	78.6	593	7	CN308959	CN308959
32	435	78.2	1107	5	BX424917	BX424917
33	433.8	78.0	960	5	BX335314	BX335314
34	433.6	78.0	795	2	BG252702	BG252702
35	432.8	77.8	968	5	BX355763	BX355763
36	432.4	77.8	681	6	CF132569	CF132569
37	427.4	76.9	948	5	BX381412	BX381412
38	424.4	76.3	999	6	CD609140	CD609140
39	421.4	75.8	588	3	BM127625	BM127625
40	421.4	75.8	818	2	BE908739	BE908739
41	419.4	75.4	869	3	BQ218607	BQ218607
42	416.2	74.9	1112	5	BX417503	BX417503
43	415.6	74.7	583	3	BP337889	BP337889
44	413	74.3	665	7	CJ016402	CJ016402
45	413	74.3	1010	1	AL541493	AL541493

ALIGNMENTS

RESULT 1
CN309034
LOCUS CN309034 659 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424711627 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
ACCESSION CN309034
VERSION CN309034.1 GI:47325448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 659 Std Error: 0.00.
FEATURES
Location/Qualifiers
1..659
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/note="oligo dt primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

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QY 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
Db |||||
QY 58 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 117
Db |||||
QY 61 CAGCGGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGACC 120
Db |||||
QY 118 CAGCGGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGAGC 177
Db |||||
QY 121 ACGGTCAACGACGTGGATTTTCAGAGTGGACGAGCCAGGCTTCATCATCAATGACTGG 180
Db |||||
QY 178 ACGGTCAACGACGTGGATTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 237
Db |||||
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCAG 240
Db |||||
QY 238 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCAG 297
Db |||||
QY 241 CTGACGCGCTGTGTTCTGTGTAATGCCCTTACTTCAACGGCGAGTGGAAAGCGCCCTTC 300
Db |||||
QY 298 CTGACACGGCTGTGTTCTGTGTAATGCCCTTACTTCAACGGCGAGTGGAAAGACTCCCTTC 357
Db |||||
QY 301 CCAGAGAAAGACACACACCGCTCTTCCACAAAGTCTGTGAGCGAGCACCGTCTCTGTG 360
Db |||||
QY 358 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCATGTCTCTGTG 417
Db |||||
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCCCGACGGCCAT 420
Db |||||
QY 418 CCCATGATGGCTCAGACCAACAAAGTTCAACTATATCTGAGTTTCCACCGCCGATGGCCAT 477
Db |||||
QY 421 TACTACGACATCCTGGAATGGCTTACCAACGCAACACTCTGAGCATGTTCATTCGCGC 480
Db |||||
QY 478 TACTACGACATCCTGGAATGGCTTACCAACGCGGACACCTCTCAGCATGTTCATTCGCTGC 537
Db |||||
QY 481 CCTACGAAAGAGGTGCTCTCTCCGCGCTTCCAGGATTTCTGAGCGCTCAGCTCATC 540
Db |||||
QY 538 CTTATGAAAGAGGTGCTCTCTCTGCGCTTCCACCAATTTCTGAGTGCAGCTCATC 597
Db |||||
QY 541 AGCCAGTGGAAAGGCA 556
Db |||||
QY 598 AGCCAGTGGAAAGGCA 613
Db |||||
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RESULT 2
BG829624
LOCUS 60276376F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899139 5',
DEFINITION mRNA sequence.
ACCESSION BG829624
VERSION BG829624.1 GI:14177211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 813)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1790 row: h column: 20
High quality sequence stop: 810.
Location/Qualifiers
1..813
/organism="Homo sapiens"
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FEATURES
source

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/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:4899139"  
/tissue_type="epithelioid carcinoma cell line"  
/lab_host="DH10B (phage-resistant)"  
/clone_lib="NIH_MGC_42"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACAG(G). Size-selected by  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH_MGC Library."
```

ORIGIN

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Query Match 81.9%; Score 455.2; DB 2; Length 813;  
Best Local Similarity 88.7%; Pred. No. 4.5e-115;  
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
QY 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60  
Db |||||  
QY 150 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 209  
Db |||||  
QY 61 CAGCGGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGACC 120  
Db |||||  
QY 210 CAGCGGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGAGC 269  
Db |||||  
QY 121 ACGGTCAACGACGTGGATTTTCAGAGTGGACGAGCCAGGCTTCATCAATGACTGG 180  
Db |||||  
QY 270 ACGGTCAACGACGTGGATTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 329  
Db |||||  
QY 191 GTGAAGAGACACACAAAAGGATGATCAATGACTTATCTTGGCCAAAGGGCTGTGACACAG 240  
Db |||||  
QY 330 GTGAAGAGACACACAAAAGGATGATCAATGACTTATCTTGGGAAAGGAGCGGTGACACAG 389  
Db |||||  
QY 241 CTGACGCGCTGTGTTCTGTGTAATGCCCTTACTTCAACGGCGAGTGGAAAGCGCCCTTC 300  
Db |||||  
QY 390 CTGACGCGCTGTGTTCTGTGTAATGCCCTTACTTCAACGGCGAGTGGAAAGACTCCCTTC 449  
Db |||||  
QY 301 CCAGAGAAAGACACTCACACCGCTCTTCCACAAAGTCTGATGGCAGCACCGTCTCTGTG 360  
Db |||||  
QY 450 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACATGTCTCTGTG 509  
Db |||||  
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTGAGTTTTCACCCCGACGGCCAT 420  
Db |||||  
QY 510 CCCATGATGGCTCAGACCAACAAAGTTCAACTATATCTGAGTTTCAACCGCCGATGGCCAT 569  
Db |||||  
QY 421 TACTACGACATCTCGGAATTCCTTACCAGCGCAACACTCTGAGCATGTTCATTCGCGCC 480  
Db |||||  
QY 570 TACTACGACATCTCGGAATTCCTTACCAGCGGACACCCCTCAGCATGTTCATTCGCGC 629  
Db |||||  
QY 481 CCCTACGAAAAAGAGGTGCTCTCTCCGCGCTTCCAGCATTTCTGAGCGCTCAGCTCATC 540  
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QY 630 CTTATGAAAGAGGTGCTCTCTCTGCGCTTCCACCAATTTCTGAGTGCAGCTCATC 689  
Db |||||  
QY 541 AGCCAGTGGAAAGGCA 556  
Db |||||  
QY 690 AGCCAGTGGAAAGGCA 705  
Db |||||
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RESULT 3
BE905905

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BE905905

601495570F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897737 5',

mRNA sequence.

BE905905

BE905905.1 GI:10399246

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 932)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM9692 row: k column: 18

High quality sequence stop: 672.

Location/Qualifiers

1. .932

FEATURES

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3897737"

/tissue_type="epithelioid carcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_70"

/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.1 kb. Library constructed by Life

Technologies."

ORIGIN

Query Match

Best Local Similarity

Matches 493; Conservative

0; Mismatches 63; Indels 0; Gaps 0;

Score 455.2; DB 2; Length 932;

Pred. No. 4.7e-115;

Location/Qualifiers

1. .1027

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOD1021YN07"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

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Qy 481 CCTTACGAAAAAGAGTGCTCTCTCGGCTTCCACGCAATTTCTGACGCTCAGTCTCATC 540
Db 914 CCTTATGAAAAAGAGTGCTCTCTCGGCTTCCACCAATTTCTGAGTGTTCGCGCATC 973
Qy 541 AGCCAGTGGAAAGGGA 556
Db 974 AGCCACTGGAAAGGCA 989

RESULT 5
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LOCUS Pan troglodytes SERPINE1 gene, VIRTUAL TRANSCRIPT, partial
DEFINITION sequence, genomic survey sequence.
ACCESSION AY402982
VERSION AY402982.1 GI:39758965
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE 1 (bases 1 to 1168)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1168)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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gene

ORIGIN

Query Match 81.9%; Score 455.2; DB 10; Length 1168;
Best Local Similarity 88.7%; Pred. No. 5e-115;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 1 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 366
Qy 61 CAGCGGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTCTTTCAGGCTGTTCGGACC 120
Db 367 CAGCGGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTTCTTTCAGGCTGTTCGGAGC 426

Qy 121 ACGGTCAAGCAGGTGGATTTTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
Db 427 ACGGTCAAGCAGGTGGATTTTTTTCAGAGATGGAGAGAGCCAGATTCATCATCAATGACTGG 486
Qy 181 GTGAAGAGACACACAAAAGGATGATCAATGATTTACTTGGCCAAAGGGCTGTGTGACCGAG 240
Db 487 GTGAAGAGACACACAAAAGGATGATCAGCAACTTGTCTTGGAAAAGGAGCGGTGGACCGAG 546
Qy 241 CTGACGCGCTGTGTCTGTGAATGCCCTCTACTTCAAGGGCCAGTGGAAACGCCCTTC 300
Db 547 CTGACACGCGCTGTGTGTGAATGCCCTCTACTTCAAGGGCCAGTGGAAAGACTCCCTTC 606
Qy 301 CCAGAGAAAAGCACTCACACCGCTCTTCCACAAAGTCTGATGGCAGCACCGCTCTCTGTG 360
Db 607 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 666
Qy 361 CCTATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTGTTCACCCCGACGCGCAT 420
Db 667 CCTATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTGTTCACCAACACTCTGAGTGTCCGATGCGCAT 726
Qy 421 TACTACGACATCTCTGGAATTCCTTACCACGGCACACTCTGAGCATCTTCATTTCCGCC 480
Db 727 TACTACGACATCTCTGGAATTCCTTACCACGGGACACCTCAGCATGTTTCATTTCTGCC 786
Qy 481 CCTTACGAAAAAGAGTGCTCTCTCGGCTTCCACGCAATTTCTGACGCTCAGTCTCATC 540
Db 787 CCTTATGAAAAAGAGTGCTCTCTCGGCTTCCACCAACACTCTGAGTGTCCGATGCGCATC 846
Qy 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCACTGGAAAGGCA 862

RESULT 6
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LOCUS Homo sapiens SERPINE1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY402981
VERSION AY402981.1 GI:39758964
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1209)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1209)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1. .1209
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ORIGIN

Query Match 81.9%; Score 455.2; DB 10; Length 1209;
Best Local Similarity 88.7%; Pred. No. 5e-115;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGACGGCGGATGCATCTTCGTG 60
DB |||||
QY 307 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGACGGCGGATGCATCTTCGTG 366
DB |||||

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGCGAAC 120
DB |||||

QY 367 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGCGAAC 426
DB |||||

QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACCGGATTCATCAATGACTGG 180
DB |||||

QY 427 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACCGGATTCATCAATGACTGG 486
DB |||||

QY 181 GTGAAGAGACACAAAGAGCATGATCAATGACTTCTTTCAGGCGGAGCGGTGGACCCAG 240
DB |||||

QY 487 GTGAAGAGACACAAAGAGCATGATCAATGACTTCTTTCAGGCGGAGCGGTGGACCCAG 546
DB |||||

QY 241 CTGACGCGCTGGTCTGTGGTGAATGCCCTTCTTTCAGGCGGAGCGGTGGACCCAG 300
DB |||||

QY 547 CTGACGCGCTGGTCTGTGGTGAATGCCCTTCTTTCAGGCGGAGCGGTGGACCCAG 606
DB |||||

QY 301 CAGAGAAAGCATCACACCGGCTTCTTTCAGGCGGAGCGGTGGACCCAG 360
DB |||||

QY 607 CCGGACTCCAGCACCCACCGGCTTCTTTCAGGCGGAGCGGTGGACCCAG 666
DB |||||

QY 361 CCGGACTCCAGCACCCACCGGCTTCTTTCAGGCGGAGCGGTGGACCCAG 420
DB |||||

QY 667 CCGGACTCCAGCACCCACCGGCTTCTTTCAGGCGGAGCGGTGGACCCAG 726
DB |||||

QY 421 TACTAGCATCTCTGGAATGCGCTTACCAGCGCAACACTCTGAGCATGTTTCATTCGCGC 480
DB |||||

QY 727 TACTAGCATCTCTGGAATGCGCTTACCAGCGCAACACTCTGAGCATGTTTCATTCGCGC 786
DB |||||

QY 481 CCTTATGAAAAGAGTGGCTCTCTCGGCTTCCAGCAATTCGAGCGCTCAGCTCATC 540
DB |||||

QY 787 CCTTATGAAAAGAGTGGCTCTCTCGGCTTCCAGCAATTCGAGCGCTCAGCTCATC 846
DB |||||

QY 541 AGCCAGTGGAAAGGGA 556
DB |||||

QY 847 AGCCAGTGGAAAGGGA 862
DB |||||

RESULT 7

CR614829
LOCUS
DEFINITION
full-length cDNA clone CS0D1031YB21 of Placenta Cot 25-normalized

ACCESSION CR614829

VERSION CR614829.1

KEYWORDS HT; CNSLT_CDNA.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1474)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue

Genoscope.

2 (bases 1 to 1474)

Direct Submission

TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

source
1. 1474
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1031YB21"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 81.9%; Score 455.2; DB 4; Length 1474;
Best Local Similarity 88.7%; Pred. No. 5.2e-115;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGACGGCGGATGCATCTTCGTG 60
DB 434 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGACGGCGGATGCATCTTCGTG 493
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGCGAAC 120
DB 494 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGCGAAC 553
QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACCGGATTCATCAATGACTGG 180
DB 554 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACCGGATTCATCAATGACTGG 613
QY 181 GTGAAGAGACACAAAGAGCATGATCAATGACTTCTTTCAGGCGGAGCGGTGGACCCAG 240
DB 614 GTGAAGAGACACAAAGAGCATGATCAATGACTTCTTTCAGGCGGAGCGGTGGACCCAG 673
QY 241 CTGACGCGCTGGTCTGTGGTGAATGCCCTTCTTTCAGGCGGAGCGGTGGACCCAG 300
DB 674 CTGACGCGCTGGTCTGTGGTGAATGCCCTTCTTTCAGGCGGAGCGGTGGACCCAG 733
QY 301 CAGAGAAAGAGTGGCTCTCTCGGCTTCCAGCAATTCGAGCGCTCAGCTCATC 360
DB 734 CCGGACTCCAGCACCCACCGGCTTCTTTCAGGCGGAGCGGTGGACCCAG 793
QY 361 CCGGACTCCAGCACCCACCGGCTTCTTTCAGGCGGAGCGGTGGACCCAG 420
DB 794 CCGGACTCCAGCACCCACCGGCTTCTTTCAGGCGGAGCGGTGGACCCAG 853
QY 421 TACTAGCATCTCTGGAATGCGCTTACCAGCGCAACACTCTGAGCATGTTTCATTCGCGC 480
DB 854 TACTAGCATCTCTGGAATGCGCTTACCAGCGCAACACTCTGAGCATGTTTCATTCGCGC 913
QY 481 CCTTATGAAAAGAGTGGCTCTCTCGGCTTCCAGCAATTCGAGCGCTCAGCTCATC 540
DB 914 CCTTATGAAAAGAGTGGCTCTCTCGGCTTCCAGCAATTCGAGCGCTCAGCTCATC 973
QY 541 AGCCAGTGGAAAGGGA 556
DB 974 AGCCAGTGGAAAGGGA 989

RESULT 8

BX379573

LOCUS

DEFINITION

BX379573 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0D1031YB21 5-PRIME, mRNA sequence.

VERSION BX379573

KEYWORDS EST..

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

BX379573 1019 bp mRNA linear EST 28-APR-2004

BX379573 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0D1031YB21 5-PRIME, mRNA sequence.

VERSION BX379573

KEYWORDS EST..

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1019)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30458782.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cretnieux, CP 5706 - 91057 Evry cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4412.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODI035CF07QPl&c=4412.f.

Location/Qualifiers

1. .1019

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI035YL13"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 81.8%; Score 454.8; DB 5; Length 1019;

Best Local Similarity 88.5%; Pred. No. 6.2e-115;

Matches 492; Conservative 1; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60

DB 432 AAGGAGCTCATGGGCGGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 491

QY 61 CAGCGGAGCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTACGGCTGTTCCGGACC 120

DB 492 CAGCGGAGCTGAAGCTGGTCCAGGGCTTCATGCCCTACTTCTTACGGCTGTTCCGGAGC 551

QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180

DB 552 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 611

QY 181 GTGAAGAGACACACAAAAGGCATGATCAATGACTTACTTTGGCCAAAGGGGTGTGGACCCAG 240

DB 612 GTGAAGAGACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGAGGCGGTGGACCCAG 671

QY 241 CTGACGGGCTGTGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAACGCCCTTC 300

DB 672 CTGACACGGCTGTGTTGGTGAATGGCCCTCTACTTCAACGGCCAGTGGAAAACGCCCTTC 731

QY 301 CCAGAGAAAGCACTCACACCGCCCTTTTCCAAAGTCTGTATGGCAGCACCGTCTCTGTG 360

DB 732 CCGCACTCCAGCACCCACCGCCGCTCTTCCAAATCAGACGGCAGCATGTGTCGTG 791

QY 361 CCCATGATGGCTCAGACCAACAAGTTTCAACTACATGAGTTTTCACCCCGCAGCGCCAT 420

DB 792 CCCATGATGGCTCAGACCAACAAGTTTCAACTACTTACTTACACCGCCGATGGCCAT 851

QY 421 TACTACGACATCTGGAAATGGCCCTTACACGGCAACA CTCTGACGATGTTCATTCGGCC 480

DB 852 TACTACGACATCTGGAAATGGCCCTTACACGGGGAACA CCGCTCAGCATGTTTCAITGTGCC 911

QY 481 CCCTACGAAAAAGAGTGCTCTCTCCGCCCTCACAGGATTCCTGACGCTCAGCTCATC 540

DB 912 CCTTATGAAAAAGAGTGCTCTCTCTGCGCTCACCAACATTCGTAGTCCCGAGCTCATC 971

QY 541 AGCCAGTGGAAAGGGA 556

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Db          972 AGCCACTGGRAGGCA 987
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RESULT 9
BX335507
LOCUS   BX335507 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION
clone CS0D1015YB08 5-PRIME, mRNA sequence.
ACCESSION
BX335507
VERSION  BX335507.2 GI:46266450
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE
1 (bases 1 to 1085)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
COMMENT
  On May 1, 2003 this sequence version replaced gi:30312419.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen. This sequence belongs to sequence cluster
  4412.f
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?s=CS0D1015DA04QP1&c=4412.f.

FEATURES             Location/Qualifiers
     source            1..1085
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CS0D1015YB08"
                        /cissue_type="PLACENTA COT 25-NORMALIZED"
                        /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                        /note="1st strand cDNA was primed with a NotI-oligo(dT)
                        primer. Five prime end enriched, double-strand cDNA was
                        digested with Not I and EcoR V
                        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      81.8%; Score 454.8; DB 5; Length 1085;
Best Local Similarity 88.5%; Pred.No. 6.3e-115;
Matches 492; Conservative 1; Mismatches 63; Indels 0; Gaps 0;

QY      1  AAGGAGCTCATGGGCGGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTTCGTG 60
         |||||
Db      421 AAGGAGCTCATGGGCGGTGGAAACAAGATGAGATCAGACGGCCGATCTTTCGTG 480
         |||||

QY      61  CAGCGGGATCTGAAGCTGTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC 120
         |||||
Db      481 CAGCGGGATCTGAAGCTGTCAGGGCTTCATGCCCTACTTCTTCAGGCTGTTCCGGAGC 540
         |||||

QY      121 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGACCGAGTTCATCATCAATGACTGG 180
         |||||
Db      541 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCGAGTTCATCATCAATGACTGG 600
         |||||

QY      181 GTGAAGAGACACACAAAAAGCATGATCAATGACTTACTTGGCCCAAGGGGTGTGGACCG 240
         |||||
Db      601 GTGAAGAGACACACAAAAAGTATGATCAGCAACTTCTGGGAAAGAGCCGTGGACCG 660
         |||||

QY      241 CTGACCGGCTGTGTTCTGGTGAATGCCCTCTACTTTCACGGCCAGTGGAAACGCCCTTTC 300
         |||||
Db      661 CTGACACGGCTGTGTTCTGGTGAATGCCCTCTACTTTCACGGCCAGTGGAAAGACTCCCTTC 720
         |||||

QY      301 CCAGAGAAAAGCACTCACACCGCCTCTTCCCAAGTCTGATGGGACGACCGTCTCTGTG 360
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Db 721 CCCGACTCCAGCACCACCGCGCTCTTCCACAAATCAGAGGAGCATGTCTCTGTG 780
 Qy 361 CCCATGATGCTGAGCAACAAGTTCAACTACACTGAGTTTCCACCCCGAGCGCCAT 420
 Db 781 CCCATGATGCTGAGCAACAAGTTCAACTACACTGAGTTTCCACCCCGAGCGCCAT 840
 Qy 421 TACTACGACATCTGGAAATGCCCTACCGGCAACACTGTGAGCATGTTTCATGCGCC 480
 Db 841 TACTACGACATCTGGAAATGCCCTACCGGCAACACTGTGAGCATGTTTCATGCGCC 900
 Qy 481 CCCTACGAAAGAGGTGCTCTCTCGCCCTCACACAGCATTTGACGCTCAGCTCATC 540
 Db 901 CCTTATGAAAGAGGTGCTCTCTCGCCCTCACACAGCATTTGAGTGCAGCTCATC 960
 Qy 541 AGCCAGTGGAAAGGGA 556
 Db 961 AGCCACTGGAAAGGCA 976

RESULT 10
 BX425037
 LOCUS 1028 bp mRNA linear EST 04-MAY-2004
 DEFINITION BX425037 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA008ZC09
 5-PRIME, mRNA sequence.
 ACCESSION BX425037.2 GI:46999418
 VERSION
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1028)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT On May 15, 2003 this sequence version replaced gi:30772430.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 4412.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?b=CLOBA008ZC09RP1&c=4412.f.

FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CLOBA008ZC09"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 ORIGIN
 Query Match 81.7%; Score 454.4; DB 5; Length 1028;
 Best Local Similarity 88.3%; Pred. No. 8e-115;
 Matches 491; Conservative 2; Mismatches 63; Indels 0; Gaps 0;

Qy 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGCAGCGCCGATGCCATCTTCGTG 60
 Db 438 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGCAGCGCCGATCTTCGTG 497

Qy 61 CAGCGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTCTTTCAGGCTGTTCGGAGC 120
 Db 498 CAGCGGATCTGAAGCTGTGTCAGGGTTTCATGCCCTACTCTTTCAGGCTGTTCGGAGC 557
 Qy 121 ACGGTCAAGCAGGTGAGATTTTTCAGAGATGAGCAGAGCAGGTTTCATCATCAATGACTGG 180
 Db 558 ACGGTCAAGCAGGTGAGATTTTTCAGAGATGAGCAGAGCAGGTTTCATCATCAATGACTGG 617
 Qy 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTTACTTGGCCAAAGGGGCTGTGGACCA 240
 Db 618 GTGAAGAGACACACAAAAGGATGATCAATGACTTTACTTGGCCAAAGGGGCTGTGGACCA 677
 Qy 241 CTGACGGGCTGTGTTCTGTGTAATGCTCTTCAACGGCCAGTGGAAAAAGCCCTTC 300
 Db 678 CTGACGGGCTGTGTTCTGTGTAATGCTCTTCAACGGCCAGTGGAAAAAGCCCTTC 737
 Qy 301 CCAGAGAAAAGCACTCACCAACCGCTCTTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 360
 Db 738 CCGGACTCCAGACACCCACCGCGCTCTTCCAAATCAGACGGCAGCATGTCTCTGTG 797
 Qy 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGAGCGCCAT 420
 Db 798 CCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGAGCGCCAT 857
 Qy 421 TACTAGACATCTGGAATTCCTTACACAGGCAACACTCTGAGCATGTTTCATTCGCGCC 480
 Db 858 TACTAGACATCTGGAATTCCTTACACAGGCAACACTCTGAGCATGTTTCATTCGCGCC 917
 Qy 481 CCTACGAAAAGAGGTGCTCTCTCCGCTTCCACAGCATTTCTGACGCTCAGCTCATC 540
 Db 918 CCTATGAAAAGAGGTGCTCTCTCTGCTTCCAAACATTCAGTGCTCCAGCTCATC 977
 Qy 541 AGCCAGTGGAAAGGGA 556
 Db 978 AGCCACTGGAAAGGCA 993

RESULT 11
 BX446279
 LOCUS 1116 bp mRNA linear EST 04-MAY-2004
 DEFINITION BX446279 Homo sapiens PLACENTA Homo sapiens cDNA clone
 XCL0BA001ZE03 5-PRIME, mRNA sequence.
 ACCESSION BX446279
 VERSION BX446279.2 GI:47007413
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1116)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT On May 15, 2003 this sequence version replaced gi:30780405.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 4412.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?b=XCL0BA001ZE03RP1&c=4412.f.

FEATURES
 source
 1..1116
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="XCL0BA001ZE03"


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DEFINITION AGENCOURT 10810368 MAPcL Homo sapiens cDNA clone IMAGE:6722018 5',
mRNA sequence.
ACCESSION CA489543
VERSION CA489543.1 GI:24952334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1. (bases 1 to 894)
NHL-GMC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cyabbs-remail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14284 row: b column: 02
High quality sequence stop: 674.
FEATURES             source
     Location/Qualifiers
         1..894
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:6722018"
             /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
             hERT-HMEL, LNCaP"
             /lab_host="EMDH10B"
             /clone_lib="MAPcL"
             /notes="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
             Subtracted with brain, liver, lung, kidney and muscle.
             Directionally cloned. Priming method: oligo-dr. Average
             insert size: 1800 bp. Library amplification: 26,000 fold.
             Kristi A. Eglund, James J. Vincent, Robert Strausberg,
             Bungkok Lee, & Ira Pastan: Discovery of new breast
             cancer genes encoding membrane and secreted proteins.
             Manuscript submitted."
ORIGIN
Query Match      80.9%; Score 450; DB 6; Length 894;
Best Local Similarity 88.3%; Pred. No. 1.3e-113;
Matches 489; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY      1  AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGACGCGCCGATGCCATCTTCGTG 60
DB      298 AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGACGCGCCGATGCCATCTTCGTG 357

QY      61  CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
DB      358 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGAGC 417

QY      121 ACGGTCAACGACGTGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
DB      418 ACGGTCAACGACGTGACTTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 477

QY      181 GTGAGAGACACAAAGAGCATGATCAATGATTAATTGGCCAGAGGCGCTGTGGACCAAG 240
DB      478 GTGAGAGACACAAAGAGCATGATCAGCAACTTCTTGGGAAGAGGCGGTGGACCAAG 537

QY      241 CTGACGCGCTGTGTTCTGTTGATGTCCTTCAACGCGCCAGTGGAAAGCGCTTC 300
DB      538 CTGACACGCGCTGTGTTGTTGATGTCCTTCAACGCGCCAGTGGAAAGACTCCCTTC 597

QY      301 CCAGAGAAAGCACTCACACCGCTCTTCCCAAGTCTGTGAGGAGCAGCCGCTCTCTGTG 360
DB      598 CCGGACTCCAGCACCCACCGCGCTCTTCCCAATATCAGACGGGAGCACTGTTCTGTG 657

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QY      361 CCCATGATGCTCAGACCAACAGTTTCACTACACTGAGTTTTCACCCCGGAGGCCAT 420
DB      658 CCCATGATGCTCAGACCAACAGTTTCACTATATGAGTTTCAACCGCCGATGGCCAT 717

QY      421 TACTACGACATCTCTGGAATTCCTTACCAGGCAACACTCTGAGCATGTTTCATTGCGGCC 480
DB      718 TACTACGACATCTCTGGAATTCCTTACCAGGCAACACTCTGAGCATGTTTCATTGCGGCC 777

QY      481 CCTACGAAAGAGGTGCTCTCTCGGCTTCCAGAGCATTTCTGAGCGTCTAGCTCATC 540
DB      778 CCTATGAAAGAGGTGCTCTCTCGGCTTCCAGCAACATTTCTGAGTGCCTGAGTCCAGCTCATC 837

QY      541 AGCCAGTGGAAAGG 554
DB      838 AGCCCTTGGAAAG 851

RESULT 14
BX382561
LOCUS      1029 bp mRNA linear EST 28-APR-2004
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI082YB17 5-PRIME, mRNA sequence.
ACCESSION BX382561
VERSION BX382561.2 GI:46832678
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1. (bases 1 to 1029)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30459067.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODI082CA09QP1&c=4412.f.
FEATURES             source
     Location/Qualifiers
         1..1029
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="CSODI082YB17"
             /tissue_type="PLACENTA COT 25-NORMALIZED"
             /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
             /note="1st strand cDNA was primed with a NotI-oligo(dT)
             primer. Five prime end enriched, double-strand cDNA was
             digested with Not I and EcoR V
             sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      80.9%; Score 450; DB 5; Length 1029;
Best Local Similarity 87.4%; Pred. No. 1.3e-113;
Matches 486; Conservative 5; Mismatches 65; Indels 0; Gaps 0;

QY      1  AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGACGCGCCGATGCCATCTTCGTG 60
DB      437 AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGACGCGCGATCTTCGTG 496

QY      61  CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
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Qy	121	ACGGTCAACGAGGTGGATTTTTCAGAGATGGA	CAGAGCCAGGTTCAATCAATGACTGG	180
Db	557	ACGGTCAACGAAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCAATCAATGACTGG		616
Qy	181	GTGAAGAGACACACAAAAGGCATCATCAATCACTTACTTGGCCAAAGGGCTGTGGACCAG	240	
Db	617	GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAAGAGCGGTGGACCAG	676	
Qy	241	CTGACGGCGCTGGTTCGGTGAATGCCCTCTACTTTCAAACGGCCAGTGGAAAAAGCCCTTC	300	
Db	677	CTGACACGGCTGGTGGTGAATGCCCTCTACTTTCAAACGGCCAGTGGAAAGACTCCCTTC	736	
Qy	301	CCAGAGAAAAGCACTCACACCGGCTCTTCCAAAGTCTGATGGCAGCAGCGTCTCTGTG	360	
Db	737	CCCGACTCCAGCACCCACCGCGGCTCTTCCAAATTCAGACGGCAGCACTGTCTCTGTG	796	
Qy	361	CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTCACACCCCGCAGCGCCAT	420	
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Db	857	TACTACGACATCTCGGAATTCGCCCTACGACGGGGMAACCTCAGMATGTTCAATGCTGCC	916	
Qy	481	CCCTACGAAAAAGAGGTGCCCTCTCTCCGCCCTCACACAGCAATCTTGACGCTCAGTCTCATC	540	
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DEFINITION	BX417006 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YG11 5-PRIME, mRNA sequence.
ACCESSION	BX417006
VERSION	BX417006.2
KEYWORDS	GI:46923165
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 971)
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 13, 2003 this sequence version replaced gi:30633206.

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1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10
11. Feature 11	Source 11
12. Feature 12	Source 12
13. Feature 13	Source 13
14. Feature 14	Source 14
15. Feature 15	Source 15
16. Feature 16	Source 16
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98. Feature 98	Source 98
99. Feature 99	Source 99
100. Feature 100	Source 100

ORIGIN

Query Match	79.9%;	Score 444.4;	DB 5;	Length 971;
Best Local Similarity	88.7%;	Pred. No. 4.7e-112;		
Matches 481;	Conservative 0;	Mismatches 61;	Indels 0;	Gaps 0;
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DB	490	CAGCGGGAATCTGAAGCTGGTCCAGGGCTTCATGCCCTACTTCTTCAGGCTGTTCCGGAGC	549	
QY	121	AGGTCACAGCAGTGGATTTTTCAGAGATGGACAGGCGCAGGTTTCATCATCAATGACTGG	180	
DB	550	AGGTCACAGCAAGTGACTTTTTCAGAGTGGAGAGCCAGAGTTTCATCATCAATGACTGG	609	
QY	181	GTGAAGAGACACACAAAAGCGATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGACACAG	240	
DB	610	GTGAAGACACACAAAAGGTATGATCAGCAACTTGCCTTGGGAAAGGACCGGTGGACACAG	669	
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QY	301	CCAGAGAAAAGCACTCACACCGCCTCTTTCACAAGTCTGTATGGGACACCGCTCTCTGTG	360	
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DB	850	TACTACGACATCTCGGAATGGCCTTACACGGGACACCTCAGCATGTTTCAATTGGTGGC	909	
QY	481	CCCTACGAAAAAGAGTGGCTCTCTCTCGGCCCTCACACAGCATTTCTGGACGCTCAGCTCATC	540	
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Search completed: March 10, 2006, 02:39:58
Job time : 5645 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 22:55:45 ; Search time 3287 Seconds
(without alignments)
9615.138 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb.in.*
3: gb.env.*
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5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
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14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	1209	11 AY888695	AY888695 Synthetic
2	556	100.0	1209	11 AY889067	AY889067 Synthetic
3	556	100.0	1209	11 AY891356	AY891356 Synthetic
4	556	100.0	1209	11 AY891655	AY891655 Synthetic
5	556	100.0	1209	11 AY893400	AY893400 Synthetic
6	556	100.0	1209	11 AY893851	AY893851 Synthetic
7	556	100.0	1532	6 CQ716284	CQ716284 Sequence
8	556	100.0	1962	8 HSPAIR1	X04744 Human mRNA
9	556	100.0	2207	8 BC010860	BC010860 Homo sapi
10	556	100.0	2660	6 CQ413075	CQ413075 Sequence
11	556	100.0	2876	6 AR106060	AR106060 Sequence
12	556	100.0	2876	6 AR106066	AR106066 Sequence
13	556	100.0	2876	6 BD094083	BD094083 Sequence
14	556	100.0	2876	6 CQ776713	CQ776713 Sequence
15	556	100.0	2876	6 AR258505	AR258505 Sequence
16	556	100.0	2876	6 AR258511	AR258511 Sequence
17	556	100.0	2876	6 AR380642	AR380642 Sequence
18	556	100.0	2876	6 AX156115	AX156115 Sequence

19	556	100.0	2876	8 HUMPAI	M16006 Human plasm
20	556	100.0	2937	6 CQ861596	CQ861596 Sequence
21	556	100.0	2937	8 HUMPAIB	M14083 Human beta-
22	556	100.0	2944	6 I08667	I08667 Sequence 4
23	556	100.0	3171	6 AX281751	AX281751 Sequence
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26	554.4	99.7	1482	8 HSPAIR	X04439 Human mRNA
27	548	98.6	1187	6 CQ785751	CQ785751 Sequence
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31	459.6	82.7	844	4 AF508034	AF508034 Equus cab
32	455.2	81.9	3000	4 SSPAI1	Y11347 S. scrofa mR
33	452	81.3	2970	4 MPAI1	X58541 Mink mRNA f
34	447.6	80.5	548	4 AF074325	AF074325 Oryctolag
35	447.2	80.4	2970	4 BTPAI1MR	AF074325 Bovine mR
36	421.6	75.8	3053	6 AX827499	AX827499 Sequence
37	421.6	75.8	3053	9 RAYPAI1A	M24067 Rattus norv
38	410.4	73.8	2741	9 BC054091	BC054091 Mus muscu
39	410.4	73.8	2999	6 CQ777582	CQ777582 Sequence
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44	204.2	36.7	249	4 BTPAI1	X52906 Bovine PAI-
45	203.6	36.6	14544	6 CQ880126	CQ880126 Sequence

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AY888695 1209 bp mRNA linear SYN 22-MAR-2005
Synthetic construct Homo sapiens clone FLH031026.01X serine or
cysteine proteinase inhibitor clade B member 1 (SERPINE1) mRNA,
complete cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Cloning of human full-length CDS in Creator (TM) recombinational
vector system
Unpublished
2 (bases 1 to 1209)
Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Direct Submission
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using BD In-Fusion(TM) cloning system
between the SalI and HindIII sites of the pDNR-Dual vector.
Additional sequences in the clone: 'ACC' after SalI site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
clonally isolated and full-length sequence-verified.
Location/Qualifiers
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ORIGIN

Query Match	100.0%;	Score 556;	DB 11;	Length 1209;
Best Local Similarity	100.0%;	Prod. No. 5.1e-119;		
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Qy	1	AAGGAGCTCATGGGGCCATCGAACACAGGATGAGATCAGCACACGACACACGACGGATCTTCGTC	60	
Db	307	AAGGAGCTCATGGGGCCATCGAACACAGGATGAGATCAGCACACGACACGACGGATCTTCGTC	366	
Qy	61	CAGCGGATCTGAAGCTGTGTCAGGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGAGC	120	
Db	367	CAGCGGATCTGAAGCTGTGTCAGGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGAGC	426	
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Db	427	ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGGACGAGATTCATCATGACTGG	486	
Qy	181	GTGAAGACACACACAAAAGGTATGATCAGCAAACTTGCTGGGAAAAGAGCGCTGGACCAG	240	
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Qy	241	CTGACACGGCTGTGTGTGTAATGCCCTCTACTTCAAQGGCCAGTGGAAAGACTCCCTTC	300	
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Qy	301	CCGCACTCCAGCACCCACCGCCGCTCTTCCACAAATCAGACGGCAGCACTGTCCTGTG	360	
Db	607	CCGCACTCCAGCACCCACCGCCGCTCTTCCACAAATCAGACGGCAGCACTGTCCTGTG	666	
Qy	361	CCCATGATGCTCAGACCAACAAGTTCAACTATACTGAGTTCACACGCCGCGATGCCAT	420	
Db	667	CCCATGATGCTCAGACCAACAAGTTCAACTATACTGAGTTCACACGCCGCGATGCCAT	756	
Qy	421	TACTAGCACTCTGGAACTGCCCTACACGGGGACACCTCAGCACTGTTCACTGTGTC	480	
Db	727	TACTAGCACTCTGGAACTGCCCTACACGGGGACACCTCAGCACTGTTCACTGTGTC	786	
Qy	481	CCTTATGAAAAGAGGTGCCCTCTCTCTGCCCTCACCACAACTTCAGAGTGCCCAAGCTCATC	540	
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RESULT	2				
LOCUS	AY889067				
LENGTH	1209 bp	mRNA	linear	SYN 29-MAR-2005	
DEFINITION	Synthetic construct Homo sapiens clone FLH016840.01X serine or				

ACCESSION	AY889067.1	GI:60654586	cysteine proteinase inhibitor clade E member 1 (SERPIN1) mRNA, complete cds.
VERSION	AY889067		
KEYWORDS	Human ORF project.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 1209)		other sequences; artificial sequences.
AUTHORS	Hines, L., Rolf, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williams, J. and Labaer, J.		
TITLE	Cloning of human full-length CDS in Creator (TM) recombinational vector system		
JOURNAL	2 (bases 1 to 1209)		Unpublished
REFERENCE	Hines, L., Rolf, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williams, J. and Labaer, J.		
AUTHORS	Direct Submission		
TITLE	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA		
JOURNAL	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-bial vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.		
COMMENT			

FEATURES source

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QY	481	CCTTATGAAAAAGAGTGCTCTCTCTGCGCCTCACCAACATTTCTGAGTGGCCAGCTCATC	540	
Db	787			
QY	541	AGCCACTGGAAGGCA	556	
Db	847			
QY		AGCCACTGGAAGGCA	862	
Db				

RESULT 6

FEATURES	source
AY893851	1209 bp mRNA linear SYN 16-MAR-2005
LOCUS	
DEFINITION	Synthetic construct Homo sapiens clone FLH057231.01L serine or cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA, partial cds.
ACCESSION	AY893851
VERSION	AY893851.1 GI:60829666
KEYWORDS	Human ORF Project.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 1209) Hines, L., Taron, B., Jepson, D., Moreira, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
TITLE	Cloning of human full-length CDS FLEXGene in Gateway(TM)recombinational vector system
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1209) Hines, L., Taron, B., Jepson, D., Moreira, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
AUTHORS	Direct Submission
TITLE	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
JOURNAL	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AtB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.
COMMENT	Location/Qualifiers 1..1209 /organism="synthetic construct" /mol_type="mRNA" /db_xref="taxon:32630" /clone="FLH057231.01L" /lab_host="Escherichia coli DH5alpha T1 resistant" /note="derived from Homo sapiens first strand cDNA library from placenta and brain" 1..>1209 /gene="SERPINE1" 1..>1209 /gene="SERPINE1" /note="nexin; plasminogen activator inhibitor type 1" /codon_start=1 /transl_table=11 /product="serine or cysteine proteinase inhibitor clade E member 1" /protein_id="AA36888.1" /db_xref="GI:60829667" /translation="MQMSPALTCVLGLALFVEGSAVHPSPSYVAHLASDFGVRVFO QVAQASKDRNVVPSVGVASVLAMQLTGGTQQIOAMGPKIDDKGMAPALRLY KELMGPNKDELSTWDAIVQDRDLKVGQFMHPFLRSTYKQVDFSEVERARFLIN DWKTHTKGMINLGLKGAVDQTLRLVNLALFNGQWKTPPDPSTHRRLLFHKSDGS TVSPVMAATKGNFTTEFTTPGHYYDILELPHGDTLSMFTAAPYEKVPVLSALTN LSAQIISHWKGNMTLRLLVLKPLKFSLETFEDLRPLNLGMDTMRKQFQADPTSLSD QSEFLHVAQALQALQKVIENVESGTVASSSTAVIVSARMAPEEITMDRFLFWVRNPQT VLFMGQVNEPL"

ORIGIN

	Query Match	100.0%;	Score 556;	DB 11;	Length 1209;
	Best Local Similarity	100.0%;	Pred. NO. 5.1e-119;		
	Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AAGGAGCTCATGGGGCCATGGRACAGAGGATGAGATCAGCACCAAGCGGATCTTCGTC	60		
Db	307	AAGGAGCTCATGGGGCCATGGAACAGGATGAGATCAGCACCAAGCGGATCTTCGTC	366		
Qy	61	CAGCGGGATGTGAAGCTGTGTCAGGGGCTTCATGCCCCCACTTCTTCAGGCTGTTCGGGAGC	120		


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/notes="pot. N-glycosylation site"
misc_feature 814..816
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misc_feature 1006..1008
/notes="pot. N-glycosylation site"
ORIGIN
Query Match 100.0%; Score 556; DB 8; Length 1962;
Best Local Similarity 100.0%; Pred. No. 5,1e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGGAACAGAGATGAGATCAGCCAGACGGATCTTCGTC 60
Db 259 AAGGAGCTCATGGGCGCATGGAACAGAGATGAGATCAGCCAGACGGATCTTCGTC 318
QY 61 CAGCGGATCTGAAGCTGTCCAGGGCTTCATGCCACCTTCTCAGGCTGTTCCGGAGC 120
Db 319 CAGCGGATCTGAAGCTGTCCAGGGCTTCATGCCACCTTCTCAGGCTGTTCCGGAGC 378
QY 121 ACGETCAAGCAAGTGGATTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATGCTGG 180
Db 379 ACGETCAAGCAAGTGGATTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATGCTGG 438
QY 181 GTGAAGACACACAAAGATGATCAGCAACTTGTGGGAAAGAGCCGTGGACCCAG 240
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QY 301 CCGACTCCAGCACCCACCGCCCTCTTCCACAAATCAGACGGCAGCACTGCTCTGTG 360
Db 559 CCGACTCCAGCACCCACCGCCCTCTTCCACAAATCAGACGGCAGCACTGCTCTGTG 618
QY 361 CCATGATGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACCGCCGATGCCCAT 420
Db 619 CCATGATGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACCGCCGATGCCCAT 678
QY 421 TACTAGCATCTCGAATCGCTTACCAGGGGACACCTCAGCATGTTTCAATGCTGCC 480
Db 679 TACTAGCATCTCGAATCGCTTACCAGGGGACACCTCAGCATGTTTCAATGCTGCC 738
QY 481 CTTTATGAAAGAGGTGCTCTCTCTGCGCTCACCACATCTGAGTCCAGGCTCATC 540
Db 739 CTTTATGAAAGAGGTGCTCTCTCTGCGCTCACCACATCTGAGTCCAGGCTCATC 798
QY 541 AGCCACTGGAAGGCA 556
Db 799 AGCCACTGGAAGGCA 814
RESULT 9
BC010860
LOCUS
DEFINITION
Homo sapiens serine (or cysteine) proteinase inhibitor, clade E
(nexin, plasminogen activator inhibitor type 1), member 1, mRNA
(CDNA clone MGC:9226 IMAGE:3893914), complete cds.
ACCESSION
BC010860
VERSION
BC010860.1 GI:14790035
SOURCE
MGC.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 2207)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toohy, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2207)

NIH MGC Project

Direct Submission

Submitted (12-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAC Plate: 14 Row: 9 Column: 15

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835158.

FEATURES

Location/Qualifiers

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/db_xref="taxon:9606"

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/tissue_type="Lung, carcinoma, large cell undifferentiated"

/clone_lib="NIH_MGC_69"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

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123..1331

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gene

CDS

TVSPVMAQTNKFNTEFTTPDGHYDILELPHGDTLSMFIAPYEKVEPLSALTNI
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ORIGIN
Query Match 100.0%; Score 556; DB 8; Length 2207;
Best Local Similarity 100.0%; Pred. No. 5.1e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCCCATGGACCAAGGATGATCAGCACACAGACCGCATCTCGTC 60
DB 429 AAGGAGCTCATGGGCCCATGGACCAAGGATGATCAGCACACAGACCGCATCTCGTC 488
QY 61 CAGCGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTCAGGCTGTTCGGAGC 120
DB 489 CAGCGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTCAGGCTGTTCGGAGC 548
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 180
DB 549 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 608
QY 181 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCGGTGACACG 240
DB 609 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCGGTGACACG 668
QY 241 CTGACACGGCTGGTGTGAATGCCCTCTACTTCAACGGCGAGTGAAGACTCCCTTC 300
DB 669 CTGACACGGCTGGTGTGAATGCCCTCTACTTCAACGGCGAGTGAAGACTCCCTTC 728
QY 301 CCGGACTCCAGACCCACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 360
DB 729 CCGGACTCCAGACCCACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 788
QY 361 CCATGATGGCTCAGACCAAGTTCACATCTACTGATTCACACCGCGAGTGGCCAT 420
DB 789 CCATGATGGCTCAGACCAAGTTCACATCTACTGATTCACACCGCGAGTGGCCAT 848
QY 421 TACTACGACATCTGGAACCTGCTTACACGGGGACACCTCAGCATGTTCACTCTGCC 480
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QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCAACATTTCTGAGTGGCCAGCTCATC 540
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QY 541 AGCCACTGGAAGGCA 556
DB 969 AGCCACTGGAAGGCA 984

RESULT 10
LOCUS CQ413075 2660 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 20146 from Patent WO0170979.
ACCESSION CQ413075
VERSION CQ413075.1 GI:41320856
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lee,J. and Lillie,J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 20146 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 5e-119;
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QY 1 AAGGAGCTCATGGGCCCATGGACCAAGGATGATCAGCACACAGACCGCATCTCGTC 60
DB 452 AAGGAGCTCATGGGCCCATGGACCAAGGATGATCAGCACACAGACCGCATCTCGTC 511
QY 61 CAGCGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTCAGGCTGTTCGGAGC 120
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DB 572 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 631
QY 181 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCGGTGACACG 240
DB 632 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCGGTGACACG 691
QY 241 CTGACACGGCTGGTGTGAATGCCCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 300
DB 692 CTGACACGGCTGGTGTGAATGCCCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 751
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DB 752 CCGGACTCCAGACCCACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 811
QY 361 CCCATGATGGCTCAGACCAAGTTCACATCTACTGATTCACACCGCGAGTGGCCAT 420
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QY 421 TACTACGACATCTGGAACCTGCTTACCAACGGGGACACCTCAGCATGTTCACTCTGCC 480
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DB 932 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCAACATTTCTGAGTGGCCAGCTCATC 991
QY 541 AGCCACTGGAAGGCA 556
DB 992 AGCCACTGGAAGGCA 1007

RESULT 11
LOCUS AR106060 2876 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6103498.
ACCESSION AR106060
VERSION AR106060.1 GI:12820125
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2876)
AUTHORS Lawrence,D.A. and Stefansson,S.P.
TITLE Mutant plasminogen activator-inhibitor type 1 (PAI-1) and uses thereof
JOURNAL Patent: US 6103498-A 1 15-AUG-2000;
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ORIGIN
Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAGGAGCTCATGGGGCCATGGAAACAAGATGAGATCAGACCAACAGACGCGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGGCCATGGAAACAAGATGAGATCAGACCAACAGACGCGATCTTCGTC 441
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCCACTTCTTCAGGCTGTTCGGAGC 120
Db 442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCCACTTCTTCAGGCTGTTCGGAGC 501
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Db 742 CCCATGATGCTCAGACCAACAAGTTCAACTATCTACTGAGTTCCACCGCCGATGGCCAT 801
QY 421 TACTAGACATCTCGAACTGCCCTACACGGGGACACCCCTCAGCATGTTTCATTTGCTGCC 480
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QY 541 AGCCACTGGAAAGGCA 556
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RESULT 12
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LOCUS AR106066 2876 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 10 from patent US 6103498.
ACCESSION AR106066
VERSION AR106066.1 GI:12820131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2876)
AUTHORS Lawrence, D.A. and Stefansson, S.P.
TITLE Mutant plasminogen activator-inhibitor type 1 (PAI-1) and uses thereof
JOURNAL Patent: US 6103498-A 10 15-AUG-2000;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2495 AAGGAGCTCATGGGGCCATGGAAACAAGATGAGATCAGACCAACAGACGCGATCTTCGTC 2436
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCCACTTCTTCAGGCTGTTCGGAGC 120
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QY 241 CTGACACGGCTGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 2255 CTGACACGGCTGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 2196
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QY 361 CCCATGATGCTCAGACCAACAAGTTCAACTATCTACTGAGTTCCACCGCCGATGGCCAT 420
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QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCCCCCTCACCAACATTCAGTGCCAGCTCATC 540
Db 2015 CTTTATGAAAAGAGTGCTCTCTCTGCCCCCTCACCAACATTCAGTGCCAGCTCATC 1956
QY 541 AGCCACTGGAAAGGCA 556
Db 1955 AGCCACTGGAAAGGCA 1940

RESULT 13
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LOCUS BD094083 2876 bp DNA linear PAT 27-AUG-2002
DEFINITION Shear stress-responsive DNAs.
ACCESSION BD094083
VERSION BD094083.1 GI:22639671
KEYWORDS WO 0125427-A/44.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2876)
AUTHORS Nojima, H., Yoshisue, H., Obayashi, M., Ota, T., Kawabata, A., Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.
TITLE Shear stress-responsive DNAs
JOURNAL Patent: WO 0125427-A 44 12-APR-2001;
KYOWA HAKKO KOGYO CO LTD, HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, AVAKO KAWABATA, KAZUHIRO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, SUMIO SUGANO
COMMENT OS Homo sapiens (human)
PN WO 0125427-A/44
PD 12-APR-2001
PF 02-OCT-2000 WO 2000JP006840
PR 01-OCT-1999 JP 99P 280976
PI HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI AVAKO KAWABATA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, KAZUHIRO SAKURADA, SUMIO SUGANO
PI SUMIO SUGANO
PC C12N15/12, C07K14/435, C07K16/18, C12P21/02, C12Q1/68, A61K38/00, A61K39/395
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FH Key Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGCACACAGAGCGCGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGCACACAGAGCGCGATCTTCGTC 441

QY 61 CAGCGGGATCTGAAGCTGGTTCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGGAGC 120
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Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCGGTGGACCCAG 621

QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
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QY 421 TACTACGACATCCTGGAATGCCCTTACCAACGGGACACCTCAGCATGTTCAATGCTGCC 480
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QY 481 CCTTATGAAAAGAGTGCTCTCTGCTCCCTCACCACATCTCAGTGCCCGAGCTCATC 540
Db 862 CCTTATGAAAAGAGTGCTCTCTGCTCCCTCACCACATCTCAGTGCCCGAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
Db 922 AGCCACTGGAAGGCA 937

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DEFINITION Sequence 399 from Patent EP1394274.
ACCESSION  CQ776713
VERSION     CQ776713.1  GI:45380103
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuwara,K.
TITLE      Methods of testing for bronchial asthma or chronic obstructive
JOURNAL    Pulmonary disease
PATENT     EP 1394274-A 399 03-MAR-2004;
Genox Research, Inc. (JP)
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CAGCGGGATCTGAAGCTGGTTCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGGAGC 120
Db 442 CAGCGGGATCTGAAGCTGGTTCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGGAGC 501

QY 121 ACGGTCGAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCAATCACTGG 180
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Db 622 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681

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QY 421 TACTACGACATCCTGGAATGCCCTTACCAACGGGACACCTCAGCATGTTCAATGCTGCC 480
Db 802 TACTACGACATCCTGGAATGCCCTTACCAACGGGACACCTCAGCATGTTCAATGCTGCC 861

QY 481 CCTTATGAAAAGAGTGCTCTCTGCTCCCTCACCACATCTCAGTGCCCGAGCTCATC 540
Db 862 CCTTATGAAAAGAGTGCTCTCTGCTCCCTCACCACATCTCAGTGCCCGAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
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RESULT 15
LOCUS      AR258505          2876 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6489143.
ACCESSION  AR258505
VERSION     AR258505.1  GI:27308859
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 2876)
AUTHORS    Lawrence,D.A. and Stefansson,S.P.
TITLE      Mutant plasminogen activator-inhibitor type 1 (PAI-1) proteins
JOURNAL    Patent: US 6489143-A 1 03-DEC-2002;
American National Red Cross; Falls Church, VA
LOCATION/Qualifiers
FEATURES   source
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Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGCACACAGAGCGCGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGCACACAGAGCGCGATCTTCGTC 441
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Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CAGCGGGATCTGAAGCTGGTTCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGGAGC 120
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QY 481 CCTTATGAAAAGAGTGCTCTCTGCTCCCTCACCACATCTCAGTGCCCGAGCTCATC 540
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QY 541 AGCCACTGGAAGGCA 556
Db 922 AGCCACTGGAAGGCA 937

RESULT 15
LOCUS      AR258505          2876 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6489143.
ACCESSION  AR258505
VERSION     AR258505.1  GI:27308859
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 2876)
AUTHORS    Lawrence,D.A. and Stefansson,S.P.
TITLE      Mutant plasminogen activator-inhibitor type 1 (PAI-1) proteins
JOURNAL    Patent: US 6489143-A 1 03-DEC-2002;
American National Red Cross; Falls Church, VA
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGCACACAGAGCGCGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGCACACAGAGCGCGATCTTCGTC 441
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Qy 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGSCTGTTCGGAGC 120
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Qy 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGAGCCAGATTTCATCAATGACTGG 180
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Qy 562 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTGTTGGAAAGAGCGGTGGACCAG 621
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Qy 682 CCCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 741
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Qy 361 CCCATGATGGCTCAGACCAAGTTCAACTATATCTAGTTTCAACGCCCGATGGCCAT 420
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Qy 742 CCCATGATGGCTCAGACCAAGTTCAACTATATCTAGTTTCAACGCCCGATGGCCAT 801
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 TACTACGACATCCTGGAACTGCCCTTACACGGGACACCCCTCAGCATGTTCTGTGCC 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 CCTTATGAAAAGAGGTGCCTCTCTGCGCTCACCAACATTTCTGAGTGCCAGCTCATC 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 862 CCTTATGAAAAGAGGTGCCTCTCTGCGCTCACCAACATTTCTGAGTGCCAGCTCATC 921
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Qy 541 AGCCACTGGAAAGGCA 556
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Job time : 3287 secs

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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 22:55:30 ; Search time 471.5 Seconds

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	556	100.0	1209	10 ADV42563	Adv42563 Human psy
4	556	100.0	1209	14 AEA81050	Aea81050 Human pla
5	556	100.0	1962	10 ACF79499	Acf79499 Human pla
6	556	100.0	2016	13 ACN41744	Acn41744 Human dia
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9	556	100.0	2860	5 ADL61934	Adl61934 Human ova
10	556	100.0	2870	6 ABV94750	Abv94750 Human pan
11	556	100.0	2876	2 AAT97303	Aat97303 Human pla
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23	556	100.0	2876	13 ADS83928	Ads83928 Human lym
24	556	100.0	2876	14 AEA81038	Aea81038 Human pla
25	556	100.0	2876	14 AEB29660	Aeb29660 Human Ser
26	556	100.0	2937	13 ADP52878	Adp52878 Drug ther
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31	555.6	100.0	2876	10 ADE48114	Ade48114 Human PAI
32	555	99.8	2876	9 ACF06144	Acf06144 Human pla
33	554.4	99.7	1482	10 AAD56136	Aad56136 Human pla
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36	553.6	99.6	3320	13 ADQ38429	Adq38429 Human SNP
37	548	98.6	1187	12 ADM41307	Adm41307 Human pla
38	541.6	97.4	1482	1 AAN81524	Aan81524 Complete
39	452	81.3	2970	10 ACF79500	Acf79500 Mink plas
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41	421.6	75.8	3053	10 ACF79503	Acf79503 Rat plasm
42	421.6	75.8	3053	10 AAD64653	Aad64653 Rat plasm
43	421.6	75.8	3053	10 ABT41815	Abt41815 Toxicity
44	421.6	75.8	3053	11 ADW21854	Adw21854 Rat hepat
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ALIGNMENTS

RESULT 1

ADF28770

ID ADF28770 standard; cDNA; 1209 BP.

XX

AC ADF28770;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human plasminogen-activator inhibitor-1 (PAI-1) encoding cDNA.

XX

KW Urokinase-type plasminogen activator; uPA;

KW plasminogen-activator inhibitor-1; PAI-1; breast cancer; tumour;

KW cancer therapy; human; ss; gene.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT

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Location/Qualifiers

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/note= "plasminogen activator inhibitor type 1"

WO2003082072-A2.

09-OCT-2003.

13-FEB-2003; 2003WO-US004538.

13-FEB-2002; 2002US-0356928P.

09-AUG-2002; 2002US-0402311P.

(HARB/) HARBECK N.

(KATE/) KATES R E.

(SCHM/) SCHMITT M.

(FOEK/) FOEKENS J A.

Harbeck N, Kates RE, Schmitt M, Foekens JA;

WPI; 2003-803930/75.

P-PSDB; ADF28771.

Selecting treatments for cancer, specifically breast cancer, based on

PT levels of urokinase and plasminogen-activator inhibitor-1 in tissue.
XX Disclosure; SEQ ID NO 3; 133pp; English.
XX
XX
CC The invention relates to selecting a treatment regime with highest
CC expected benefit to a patient with primary breast cancer. The method
CC involves measuring the levels of urokinase-type plasminogen activator
CC (uPA) and plasminogen-activator inhibitor-1 (PAI-1), or corresponding
CC mRNA, in primary tumour tissue (or a sample); and classifying the patient
CC as low risk (LR) if the uPA level is below a cut-off value of between the
CC 55 th . and 75 th percentile of normalized or analogous uPA in a
CC randomized population of breast cancer patients, and if the PAI-1 level
CC is lower than a cut-off value between the 61 st and 81 st percentile in
CC the same population, or as high risk (HR) if the levels of uPA and PAI-1
CC are above these cut-off values. The treatment of LR (or HR) patients is
CC then selected as one that results in the highest expected benefit in a
CC comparable population of LR (or HR) patients. The method is used: for
CC selection of the most effective therapy, including one designed to
CC prevent relapse; and to predict expected benefit, overall or disease-free
CC survival in patients with cancer, particularly of the breast but also
CC leukemia and plasmacytoma. The method can also be used: to predict the
CC benefit of preventative treatment for relapse of cancer, especially where
CC HR patients are treated with bisphosphonate drugs; for deciding whether
CC or not to administer an aggressive or non-aggressive regime; and for
CC deciding whether or not to administer chemotherapy in combination with
CC hormone therapy (i.e. if the patient is LR, chemotherapy is not
CC administered; in this case HR patients are those who are estrogen- and/or
CC progesterone- receptor positive). The present sequence represents a cDNA
CC encoding a human PAI-1 polypeptide.
XX

Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 10; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CAGCGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTCAGGCTGTTCGGAGC 120
DB 367 CAGCGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTCAGGCTGTTCGGAGC 426

QY 121 ACGGTCACGAGTGGCTTTTCAGGCTGGAGAGAGCCAGATTCATCAATCAATCACTGG 180
DB 427 ACGGTCACGAGTGGCTTTTCAGGCTGGAGAGAGCCAGATTCATCAATCAATCACTGG 486

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QY 301 CCCGACTCCAGCACCCAGCCGCTCTTCCAAATCAGAGCGGAGCAGCTGTCTCTGG 360
DB 607 CCCGACTCCAGCACCCAGCCGCTCTTCCAAATCAGAGCGGAGCAGCTGTCTCTGG 666

QY 361 CCCATGAGGCTCAGACCAACAAAGTTCAACTATCTAGATTCCACACGCCGATGCCAT 420
DB 667 CCCATGAGGCTCAGACCAACAAAGTTCAACTATCTAGATTCCACACGCCGATGCCAT 726

QY 421 TACTACGACATCCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAATGCTGCC 480
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DB 787 CTTATGAAAGAGTGCTCTCTCTGCCCTCACCACATCTCAGTGCCTCAGCTCATC 846

QY 541 AGCCACTGGAAAGGCA 556

DB 847 AGCCACTGGAAAGGCA 862

RESULT 2
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ID AAD64654 standard; cDNA; 1209 BP.
XX
AC AAD64654;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human plasminogen activator inhibitor-1 (PAI-1) coding region.
XX
KW Plasminogen activator inhibitor-1; PAI-1; cardiovascular disease;
KW fibrotic disease; gene therapy; antiinflammatory; gene; human; ss.
XX
OS Homo sapiens.
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FH Key Location/Qualifiers
FT 1..1209
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FT protein"
FT /note= "Capital T represents cleavage sites"
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PN US2003199463-A1.
XX
PD 23-OCT-2003.
XX
PF 23-APR-2002; 2002US-00128706.
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PR 23-APR-2002; 2002US-00128706.
XX
PA (ITES/) ITESCU S.
XX
PI Itescu S;
XX
DR WPI; 2003-852809/79.
DR P-PSDB; ABW02690.
XX

New catalytic nucleic acid that hybridizes to and specifically cleaves an mRNA encoding a Plasminogen Activator Inhibitor-1, useful in preparing a composition for treating e.g., cardiovascular or fibrotic disease.

Disclosure; SEQ ID NO 17; Opp; English.

The present invention relates to a new catalytic nucleic acid that hybridizes to and specifically cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1). The invention is useful in preparing a composition for treating cardiovascular or fibrotic disease. The invention is also used in gene therapy. The present sequence is human plasminogen activator inhibitor-1 (PAI-1) coding region

Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 10; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 60
DB 307 AAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 366

QY 61 CAGCGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTCAGGCTGTTCGGAGC 120
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QY 241 CTGACACGGTGTGCTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 547 CTGACACGGTGTGCTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
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Db 607 CCCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 666
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Db 727 TACTAGACATCTGGAAGTCCCTTACCAGGGGACACCTCAGCATGTTTCATGTCGC 786
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Db 787 CCTTATGAAAGAGGTGCTCTCTGCGCTCACCACCAACATTCAGTGCCAGCTCATC 846
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Db 847 AGCCACTGGAAGGCA 862
RESULT 3
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AC ADV42563;
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DT 10-MAR-2005 (first entry)
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KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
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OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
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PF 04-JUN-2004; 2004WO-US017686.
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PR 04-JUN-2003; 2003US-0475915P.
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PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
WPI; 2005-031682/03.
XX
DR New microarray comprising probes for genes involved in
PT psychoneuroendocrine (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 191; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrine (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrine gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.

XX
SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;
Query Match 100.0%; Score 556; DB 14; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGGAAACAAGGATGAGATCAGACACCAAGCGATCTTCGTC 60
Db 307 AAGGAGCTCATGGGCGCATGGAAACAAGGATGAGATCAGACACCAAGCGATCTTCGTC 366
QY 61 CAGCGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTTCAAGGCTGTTCCGAGC 120
Db 367 CAGCGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTTCAAGGCTGTTCCGAGC 426
QY 121 ACGGTCAAGCAAGTGGACATTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 180
Db 427 ACGGTCAAGCAAGTGGACATTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 486
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTGTGGGAAAGAGCCGTGGACAG 240
Db 487 GTGAAGACACACAAAGGTATGATCAGCAACTTGTGGGAAAGAGCCGTGGACAG 546
QY 241 CTGACACGGTGTGCTGTGTAATGCCCTTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 547 CTGACACGGTGTGCTGTGTAATGCCCTTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 360
Db 607 CCCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 666
QY 361 CCATGATGCTCAGACCAACAAAGTTCATATCTAGAGTTCCACCGCCGATGGCCAT 420
Db 667 CCATGATGCTCAGACCAACAAAGTTCATATCTAGAGTTCCACCGCCGATGGCCAT 726
QY 421 TACTAGACATCTGGAAGTCCCTTACCAGGGGACACCTCAGCATGTTTCATGTCGC 480
Db 727 TACTAGACATCTGGAAGTCCCTTACCAGGGGACACCTCAGCATGTTTCATGTCGC 786
QY 481 CCTTATGAAAGAGGTGCTCTCTGCGCTCACCACCAACATTCAGTGCCAGCTCATC 540
Db 787 CCTTATGAAAGAGGTGCTCTCTGCGCTCACCACCAACATTCAGTGCCAGCTCATC 846
QY 541 AGCCACTGGAAGGCA 556
Db 847 AGCCACTGGAAGGCA 862
RESULT 4
AEA81050
ID AEA81050 standard; cdna; 1209 BP.
XX
AC AEA81050;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human plasminogen activator inhibitor-1 encoding cdna SEQ ID NO:17.
XX
KW antisense therapy; RNA interference; plasminogen activator inhibitor-1;
KW vasotropic; thrombolytic; hemostatic; vascular disease;
KW thrombocyte disorder; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..1209
FT /*tag= a
FT /product= "plasminogen activator inhibitor-1 (PAI-1)"
XX
PN US2005148527-A1.
XX
PD 07-JUL-2005.
XX

CC improvement of a vascular thrombotic disorder, asthma, chronic
CC obstructive pulmonary disease, alopecia, undesired weight loss such as
CC anorexia, Alzheimer's disease, systemic amyloid deposition, systemic
CC amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness,
CC keloids, apocrine cysts, acne, atherosclerosis, ageing,
CC hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
XX
SQ Sequence 1962 BP; 456 A; 569 C; 505 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 10; Length 1962;
Best Local Similarity 100.0%; Pred. No. 5.8e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCAGCAGCGGATCTTCGTC 60
DB 259 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCAGCAGCGGATCTTCGTC 318

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
DB 319 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 378

QY 121 ACGGTCAAGCAAGTGAGCTTTTTCAGAGTGGAGAGCCAGATTCATCAATGATCG 180
DB 379 ACGGTCAAGCAAGTGAGCTTTTTCAGAGTGGAGAGCCAGATTCATCAATGATCG 438

QY 181 GTGAAGACACACAAAGGATGATGATCAGCAACTTGTGGAAAGAGCGGTGGACCAG 240
DB 439 GTGAAGACACACAAAGGATGATGATCAGCAACTTGTGGAAAGAGCGGTGGACCAG 498

QY 241 CTGACAGGCTGGTGGTGAATGCTTCTACTTCAAGCCAGTGGAAAGACTCCCTTC 300
DB 499 CTGACAGGCTGGTGGTGAATGCTTCTACTTCAAGCCAGTGGAAAGACTCCCTTC 558

QY 301 CCGGACTCCAGACCCACCGCGCTTCTTCCAAATCAGACGCGACACTGCTCTGTG 360
DB 559 CCGGACTCCAGACCCACCGCGCTTCTTCCAAATCAGACGCGACACTGCTCTGTG 618

QY 361 CCCATGATGCTCAGACCAAGTTCATCTACTGAGTTTCCAGCCGCGATGGCCAT 420
DB 619 CCCATGATGCTCAGACCAAGTTCATCTACTGAGTTTCCAGCCGCGATGGCCAT 678

QY 421 TACTAGGACATCTGGAACTGCCCTTACCGGGGACACCTCTAGCATGTTTCTGTCGC 480
DB 679 TACTAGGACATCTGGAACTGCCCTTACCGGGGACACCTCTAGCATGTTTCTGTCGC 738

QY 481 CTTTATGAAAGAGTGCTCTCTCTGCGCTTCCCAATTCAGATGCGCCAGCTCATC 540
DB 739 CTTTATGAAAGAGTGCTCTCTCTGCGCTTCCCAATTCAGATGCGCCAGCTCATC 798

QY 541 AGCCACTGGAAAGGCA 556
DB 799 AGCCACTGGAAAGGCA 814

RESULT 6
ACN41744
ID ACN41744 standard; cDNA; 2016 BP.
XX
AC AC
XX
ACN41744;
DT
18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:619.
XX
KW ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX

PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
PA
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Garstin EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LI;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Pollock JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX
WPI; 2004-329368/30.
P-PSDB; ABM83092.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2016 BP; 464 A; 628 C; 508 G; 416 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 13; Length 2016;
Best Local Similarity 100.0%; Pred. No. 5.8e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCAGCAGCGATCTTCGTC 60
DB 429 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCAGCAGCGATCTTCGTC 488

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
DB 489 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 548

QY 121 ACGGTCAAGCAAGTGAGCTTTTTCAGAGTGGAGAGCCAGATTCATCAATGATCG 180
DB 549 ACGGTCAAGCAAGTGAGCTTTTTCAGAGTGGAGAGCCAGATTCATCAATGATCG 608

QY 181 GTGAAGACACACAAAGGATGATGATCAGCAACTTGTGGAAAGAGCGGTGGACCAG 240
DB 609 GTGAAGACACACAAAGGATGATGATCAGCAACTTGTGGAAAGAGCGGTGGACCAG 668

QY 241 CTGACAGGCTGGTGGTGAATGCTTCTACTTCAAGCCGCGATGGAAAGACTCCCTTC 300
DB 669 CTGACAGGCTGGTGGTGAATGCTTCTACTTCAAGCCGCGATGGAAAGACTCCCTTC 728

QY 301 CCGGACTCCAGACCCACCGCGCTTCTTCCAAATCAGACGCGGACACTGCTCTGTG 360
DB 729 CCGGACTCCAGACCCACCGCGCTTCTTCCAAATCAGACGCGGACACTGCTCTGTG 788

XX 23-MAY-2003; 2003US-0473238P.
PR 27-FEB-2004; 2004US-0548299P.
XX (GETH) GENENTECH INC.
XX Phillips H;
XX WPI; 2005-048766/05.
DR P-PSDB; ADV70216.
XX Treating a mammal having a tumor of glial origin comprising cells that
PT express a type A or B glial tumor antigen by contacting the cells with a
PT composition comprising first and second binding agents.
XX Disclosure; SEQ ID NO 45; 374pp; English.
XX
XX The invention describes a method of treating a mammal having a tumor of
CC glial origin comprising cells that express a type A or B glial tumor
CC antigen comprising contacting the cells with a composition of: a first
CC binding agent comprising a first antibody, oligopeptide or organic
CC molecule that binds to a type A or B glial tumor antigen; and a second
CC binding agent comprising a second antibody, oligopeptide or organic
CC molecule that binds to a type B or A glial tumor antigen. Also described
CC is a method of determining the presence of a type A or B glial tumor in a
CC mammal. The method is useful in treating a mammal having a tumor of glial
CC origin comprising cells that express a type A or B glial tumor antigen.
CC This sequence represents a human tumor-associated antigenic target
CC polynucleotide.
XX
SQ Sequence 2177 BP; 515 A; 638 C; 553 G; 471 T; 0 U; 0 Other;
Query Match 100.0%; Score 556; DB 14; Length 2177;
Best Local Similarity 100.0%; Pred. No. 6e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGTGAACAAAGATGATCAGACACACACGCGATCTTCGTC 60
DB 414 AAGGAGCTCATGGGCGCATGTGAACAAAGATGATCAGACACACACGCGATCTTCGTC 473
QY 61 CAGCGGGATCTGAAGCTGGTTCAGAGGCTTCATGCCCTCTCTTCAAGGCTGTTCCGGAGC 120
DB 474 CAGCGGGATCTGAAGCTGGTTCAGAGGCTTCATGCCCTCTCTTCAAGGCTGTTCCGGAGC 533
QY 121 AGGTCAGCAAGTGACATTTTCAGAGGTGGAGAGCCAGATTCATCATATGACTGG 180
DB 534 AGGTCAGCAAGTGACATTTTCAGAGGTGGAGAGCCAGATTCATCATATGACTGG 593
QY 181 GTGAACACACACAAAGATGATCAGCACTTCTTGGGAAAGGAGCGGTGGACACG 240
DB 594 GTGAACACACACAAAGATGATCAGCACTTCTTGGGAAAGGAGCGGTGGACACG 653
QY 241 CTGACACGGCTGGTGGTGAATGCTCTTCAACGGCCAGTGGAGACTCCCTTC 300
DB 654 CTGACACGGCTGGTGGTGAATGCTCTTCAACGGCCAGTGGAGACTCCCTTC 713
QY 301 CCGGACTCCAGACACCCACCGCGCTCTTCCAAATCAGACGGCAGCTGTCTGTG 360
DB 714 CCGGACTCCAGACACCCACCGCGCTCTTCCAAATCAGACGGCAGCTGTCTGTG 773
QY 361 CCATGATGGCTCAGACACCAAGTTCATATATAGTTCACACGCCGATGCCAT 420
DB 774 CCATGATGGCTCAGACACCAAGTTCATATATAGTTCACACGCCGATGCCAT 833
QY 421 TACTACGATCTGGAACTGGCTTACACGGGACACCTCAGCATGTTTCATGTCG 480
DB 834 TACTACGATCTGGAACTGGCTTACACGGGACACCTCAGCATGTTTCATGTCG 893
QY 481 CTTTATGAAAAAGAGTGCTCTCTTCGCCCTCACCAACATTCAGTGCCCGAGCTCATC 540
DB 894 CTTTATGAAAAAGAGTGCTCTCTTCGCCCTCACCAACATTCAGTGCCCGAGCTCATC 953
QY 541 AGCCACTGGAAAGGCA 556

Db 954 AGCCACTGGAAAGGCA 969

RESULT 9

ADL61934
ID ADL61934 standard; DNA; 2660 BP.
XX
AC ADL61934;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #20146.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.

Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

Disclosure; SEQ ID NO 20146; 106pp; English.

The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence of the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the

Db 796 TACTACGACATCTGGAACTGCTACACAGGGGACACCCCTCAGCATGTTCTGCTGCC 855
 QY 481 CCTTATGAAAAGAGGTGGCTCTCTGCGCTTACCAACATTCAGTGGCCCGAGCTCATC 540
 Db 856 CCTTATGAAAAGAGGTGGCTCTCTGCGCTTACCAACATTCAGTGGCCCGAGCTCATC 915
 QY 541 AGCCACTGGAAGGCA 556
 Db 916 AGCCACTGGAAGGCA 931

RESULT 11

AAT97303

ID AAT97303 standard; DNA; 2876 BP.

XX

AC AAT97303;

XX

DT 14-APR-1998 (first entry)

XX

DE Human plasminogen activator inhibitor DNA.

XX

KW Plasminogen activator inhibitor type 1; PAI-1; human; elastase inhibitor;
 KW vitronectin; cell attachment; cell migration; cell proliferation;
 KW emphysema; adult respiratory distress syndrome; acute lung inflammation;
 KW alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis;
 KW pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis;
 KW restenosis; neointima; fibrosis; wound healing; tumour; metastasis;
 KW psoriasis; thrombosis; angiogenesis; therapy; ds.

XX Homo sapiens.

OS

XX

FH Key

FT CDS

FT

FT sig_peptide

FT

FT mat_peptide

FT

XX

PN W09739028-A1.

XX

PD 23-OCT-1997.

XX

PF 11-APR-1997; 97NO-US006071.

XX

PR 12-APR-1996; 96US-0015299P.

XX

PA (AMNA-) AMERICAN NAT RED CROSS.

XX

PI Lawrence DA, Stefansson SP;

XX

DR WPI; 1997-526399/48.

XX

DR P-PSDB; AAW31587.

XX

PT Plasminogen activator-inhibitor type I mutant inhibits elastase - or has

PT high affinity for vitronectin, for therapeutic inhibition of elastase or

PT vitronectin-mediated cell attachment, migration etc.

XX

PS Disclosure; Page 91-95; 144pp; English.

XX

CC This nucleotide sequence codes for wild-type human plasminogen activator
 CC inhibitor type (PAI-1) (see AAW31587). Novel mutants (see AAW26710-25) of
 CC the PAI-1 mature protein are claimed that inhibit elastase or other
 CC elastase-like proteases, or are inhibitors of vitronectin-dependent cell
 CC migration. The mutants are obtained by site-directed mutagenesis of the
 CC PAI-1 DNA sequence and expression in host cells, and have a range of
 CC therapeutic uses

XX

SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 2; Length 2876;

Best Local Similarity 100.0%; Pred. No. 6.5e-137;

XX

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGCACCCAGACGGAGCTTCTGTC 60
 Db 382 AAGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGCACCCAGACGGAGCTTCTGTC 441
 QY 61 CAGGGGATCTGAAGCTGGTCCAGGGGCTTCATGCCCACTTCTTCAAGGCTGTTCCGGAGC 120
 Db 442 CAGGGGATCTGAAGCTGGTCCAGGGGCTTCATGCCCACTTCTTCAAGGCTGTTCCGGAGC 501
 QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 180
 Db 502 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 561
 QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGAGCCGTTGGACCAG 240
 Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGAGCCGTTGGACCAG 621
 QY 241 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGGAGACTCCCTTC 300
 Db 622 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGGAGACTCCCTTC 681
 QY 301 CCGAGCTCCAGCACCCACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTGTG 360
 Db 682 CCGAGCTCCAGCACCCACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTGTG 741
 QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTACCAACGCCGATGGCCAT 420
 Db 742 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTACCAACGCCGATGGCCAT 801
 QY 421 TACTAGCATCTCTGGAATGCCCTTACACGGGACACCCCTCAGCATGTTCAATTTGTC 480
 Db 802 TACTAGCATCTCTGGAATGCCCTTACACGGGACACCCCTCAGCATGTTCAATTTGTC 861
 QY 481 CCTTATGAAAAGAGTGGCTCTCTGCGCTCACCACCAACTTGTAGTGGCCAGCTCATC 540
 Db 862 CCTTATGAAAAGAGTGGCTCTCTGCGCTCACCACCAACTTGTAGTGGCCAGCTCATC 921
 QY 541 AGCCACTGGAAGGCA 556
 Db 922 AGCCACTGGAAGGCA 937

RESULT 12
 AAS09460
 ID AAS09460 standard; cDNA; 2876 BP.
 XX
 AC AAS09460;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Human cDNA encoding Plasminogen activator inhibitor-1, PAI-1.
 KW Human; Plasminogen activator inhibitor-1; PAI-1; serpin;
 KW immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome;
 KW ARDS; HIV infection; Human immunodeficiency virus; prostate cancer;
 KW TNF-mediated inflammation; benign prostatic hypertrophy; ss.
 XX
 OS Homo sapiens.

FH Key
 FT CDS
 FT
 FT sig_peptide
 FT
 FT sig_peptide
 FT
 FT mat_peptide
 FT
 FT

Location/Qualifiers
 76..1284
 /tag= a
 /product= "PAI-1"
 76..143
 /tag= c
 /note= "Alternative signal peptide"
 76..138
 /tag= b
 /note= "Alternative signal peptide"
 139..1281
 /tag= d
 /label= Mature_PAI_1 #1

FT mat_peptide /note= "Both forms of the protein are detected in vivo"
FT 144. .1281 /*tag= e
FT /label= Mature_PAI_1 #2
FT /note= "Both forms of the protein are detected in vivo"
XX
PN WO200138560-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US032315.
XX
XX 22-NOV-1999; 99US-0167553P.
XX
XX (AMNA-) AMERICAN NAT RED CROSS.
XX
XX Lawrence DA, Day D;
XX
XX WPI; 2001-441438/47.
XX P-PSDB; AAU04913.
XX
XX Detecting a functionally active form of an enzyme in a biological sample
XX comprises contacting an enzyme inhibitor immobilized on a solid
XX substrate.
XX
XX Disclosure; Fig 3; 69pp; English.
XX
XX The sequence encodes human plasminogen activator inhibitor-1, PAI-1, a
XX serine proteinase inhibitor or serpin. The protein is used to demonstrate
XX the method of the invention which comprises detecting a functionally
XX active form of an enzyme in a biological sample by contacting an enzyme
XX inhibitor immobilised on a solid substrate with the biological sample and
XX measuring the binding of the enzyme inhibitor to the active form of the
XX enzyme by a detectable label, where the enzyme inhibitor specifically
XX forms a covalent bond or binds with a dissociation constant of 1 x 10⁻⁹M
XX or less with the active form of the enzyme. The present invention
XX provides a sensitive method for the detection of a functionally active
XX form of an enzyme in a biological sample. Human PAI-1 can be used to
XX detect a number of enzymes including tissue plasminogen activator,
XX urokinase, thrombin, plasmin, neurophil elastase, pancreatic elastase,
XX trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as
XX such can be used in methods to diagnose diseases such as cystic fibrosis,
XX acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated
XX inflammation, prostate cancer and benign prostatic hypertrophy
XX
XX Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 556; DB 4; Length 2876;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 60
DB 382 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 441
QY 61 CAGCGGGATCTGAAGCTGGTCCAGCGCTTCATGCCCTTCTTCAGGCTGTTCGGAGC 120
DB 442 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCTTCTTCAGGCTGTTCGGAGC 501
QY 121 ACGGTCAAGCAAGTGAGCTTTTTCAGAGGTGGAGAGCGCAGATTTCATCATCAATGACTGG 180
DB 502 ACGGTCAAGCAAGTGAGCTTTTTCAGAGGTGGAGAGCGCAGATTTCATCATCAATGACTGG 561
QY 181 GTGAGACACACACAAAGGTTATGATCAGCACTTCTTGGGAAGGAGCGGTGGACACAG 240
DB 562 GTGAGACACACACAAAGGTTATGATCAGCACTTCTTGGGAAGGAGCGGTGGACACAG 621
QY 241 CTGACACGGCTGGTGGTGAATGCCCTTCTACTTCAACGGGCAGTGGGAAGACTCCCTTC 300
DB 622 CTGACACGGCTGGTGGTGAATGCCCTTCTACTTCAACGGGCAGTGGGAAGACTCCCTTC 681
QY 301 CCCGACTTCAGACCCACCGCCGCTCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 360
|||||

DB 682 CCCGACTTCAGACCCACCGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 741
QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTTCACACGCCCGATGCCCAT 420
DB 742 CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTTCACACGCCCGATGCCCAT 801
QY 421 TACTACGACATCTCTGGAACTGCCCTTACACCGGGGACACCTTCAGCATGTTTCATTCGTC 480
DB 802 TACTACGACATCTCTGGAACTGCCCTTACACCGGGGACACCTTCAGCATGTTTCATTCGTC 861
QY 481 CTTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACATCTCTGAGTGGCCAGCTCATC 540
DB 862 CTTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACATCTCTGAGTGGCCAGCTCATC 921
QY 541 AGCCACTGGAAGGCA 556
DB 922 AGCCACTGGAAGGCA 937
RESULT 13
AAH02917
ID AAH02917 standard; DNA; 2876 BP.
XX
XX AC AAH02917;
XX
XX DT 15-JUN-2001 (first entry)
XX
XX DE Human shear stress-response coding sequence SEQ ID NO: 87.
XX
XX KW Human; shear stress-response protein; vascular disease; arteriosclerosis;
XX ds.
XX
XX OS Homo sapiens.
XX
XX FN WO200125427-A1.
XX
XX PD 12-APR-2001.
XX
XX PF 02-OCT-2000; 2000WO-JP006840.
XX
XX PR 01-OCT-1999; 99JP-00280976.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX PA (NOJII/) NOJIMA H.
XX
XX PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
XX DR WPI; 2001-266308/27.
XX P-PSDB; AAB90794.
XX
XX PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis.
XX
XX PS Claim 20; Page 472-476; 678pp; Japanese.
XX
XX CC The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension
XX
XX SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;
Query Match 100.0%; Score 556; DB 4; Length 2876;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 60
DB 382 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 441

Qy	61	CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCCACTTCTTCAAGGCTGTTCCGGAGC	120
Db	442	CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCCACTTCTTCAAGGCTGTTCCGGAGC	501
Qy	121	ACGGTCAAGCAAGTGGACATTTTTCAGAGTGGAGAGAGCCAGATTATCATCAATGACTGG	180
Db	502	ACGGTCAAGCAAGTGGACATTTTTCAGAGTGGAGAGAGCCAGATTATCATCAATGACTGG	561
Qy	181	GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTTGGAAAAGGAGCCGTGGACCAG	240
Db	562	GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTTGGAAAAGGAGCCGTGGACCAG	621
Qy	241	CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	300
Db	622	CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	681
Qy	301	CCCGACTCCAGCACCCACGGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG	360
Db	682	CCCGACTCCAGCACCCACGGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG	741
Qy	361	CCCATGATGGCTCAGACCAACAAAGTTTCAACTATACTGAGTTTCACCACGCCCGATGGCCAT	420
Db	742	CCCATGATGGCTCAGACCAACAAAGTTTCAACTATACTGAGTTTCACCACGCCCGATGGCCAT	801
Qy	421	TACTACGACATCTCTGGAACTGCCCTACCAACGGGGACACCCCTCAGCATGTTCAATGCTGCC	480
Db	802	TACTACGACATCTCTGGAACTGCCCTACCAACGGGGACACCCCTCAGCATGTTCAATGCTGCC	861
Qy	481	CTTTATGAAAAGAGGTGCCTCTCTCTGCCCTCACCAACATTTCTGAGTGCACAGTCTCATC	540
Db	862	CTTTATGAAAAGAGGTGCCTCTCTCTGCCCTCACCAACATTTCTGAGTGCACAGTCTCATC	921
Qy	541	AGCCACTGGAAAGGCA	556
Db	922	AGCCACTGGAAAGGCA	937

RESULT 14

ABV77991
ID ABV77991 standard; DNA; 2876 BP.

XX
AC ABV77991:

DT 12-NOV-2002 (first entry)

DE Hypoxia-regulated protein coding sequence #11.

Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; anti-inflammatory; vulnery; gynecological; ophthalmological; vaccine; KW
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer; KW
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress; KW
KW preclampsia; atherosclerosis; inflammatory condition; wound healing; KW
KW inflammation; erythropoiesis; hair loss; human; gene; ds. KW

OS Homo sapiens.

AA
PN
WO200246465-A2.

13-JUN-2002

PF 10-DEC-2001; 2001WO-GB005458.

AA
PR 08-DEC-2000: 2000GB-00030076.

PR 08-FEB-2001; 2001GB-00003156.
PR 25-OCT-2001; 2001GB-00025666

XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.

AA White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI PI Rayner WN;

DR WPI; 2002-627238/67.

RESULT 15

PT Identifying a gene involved in disease for treating hypoxia-regulated
PT conditions, comprises comparing the transcriptome/proteome of two cell
PT types under different conditions and identifying a differentially
PT regulated gene.

PS Claim 37; Page 338; 538pp; English.

The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV77873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumorigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preclapmia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss.

Sequence 2876 BP: 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;

SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 6; Length 2876;

Best Local Similarity 100.0%; Pred. No. 6.5e-137;

Matches	556;	Conservative	0;	Mismatches	0;	Indels	0
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QY 1 AAGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGACCAACAGACGCGATCTTTCGTC 60

Db
382 AAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGACCACACAGACGGATCTTCGTC 441

05 61 CAGCGGATCTTGAGAGCTGGTCACGGCGTTCTATGCCCCACCTGCTTCTACGCTGCTTCCCCAC

100

TOTAL

QY 121 ACGGTCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTCAATCAATCAATGACTTGG 180

Db
502 ACGGTCAAGCAAGTGGACTTTTCAGAGGGTGGAGAGAGCCAGATTTCATCATCAATGACTGG 561

QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGCTTGGAAAGGAGCCGTGGACCAG 240

Db
562 GTGAAGACACACACAAAGGTATGATCAGCAACTTGCTTGGAAAGGAGCCGTGGACCAG 621

241 CTGACACGGCTGGTGGATGCCCTCTACTTCAACGGCCAGTGGAGA CTCCCTTC 300

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QY 541 AGCCACTGGAAGGCA 556

Db 922 AGCCACTGGAAGGCA 937

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:40 ; Search time 141.5 Seconds
(without alignments)
6984.624 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88878028 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	2876	3	US-08-840-204-1
2	556	100.0	2876	3	US-08-840-204-10
3	556	100.0	2876	3	US-09-324-494A-1
4	556	100.0	2876	3	US-09-324-494A-10
5	556	100.0	2876	3	US-09-023-655-1187
6	114	20.5	1191	3	US-09-016-434-1210
7	114	20.5	2029	9	5187089-1
8	114	20.5	2029	9	5457090-1
9	114	20.5	2029	9	5495001-6
10	114	20.5	2032	9	5187089-3
11	114	20.5	2032	9	5457090-3
12	110.8	19.9	2031	9	5495001-8
13	70.8	12.7	1316	2	US-07-755-461A-12
14	70.6	12.7	1328	2	US-07-679-052A-14
15	70.6	12.7	1340	2	US-07-679-052A-16
16	70.6	12.7	1482	2	US-07-768-286B-5
17	70.6	12.7	1512	2	US-07-768-286B-3
18	70.6	12.7	1610	2	US-07-768-286B-1
19	70.6	12.7	1854	3	US-09-023-655-1189
20	70.6	12.7	1884	3	US-09-023-655-1188
21	70.6	12.7	2409	2	US-07-911-531-18
22	70.6	12.7	2409	2	US-07-693-636A-18
23	70	12.6	1185	3	US-09-023-339-3
24	70	12.6	1260	3	US-09-023-173-5

25	70	12.6	1308	3	US-09-023-173-10	Sequence 10, Appl
26	70	12.6	1308	3	US-09-023-339-6	Sequence 6, Appl
27	69.2	12.4	1152	2	US-08-315-831A-13	Sequence 13, Appl
28	69.2	12.4	1152	2	US-08-662-318-13	Sequence 13, Appl
29	69.2	12.4	1152	6	PCT-US95-12509-13	Sequence 13, Appl
30	69.2	12.4	1316	2	US-08-315-831A-12	Sequence 12, Appl
31	69.2	12.4	1316	2	US-08-662-318-12	Sequence 12, Appl
32	69.2	12.4	1316	6	PCT-US95-12509-12	Sequence 12, Appl
33	69.2	12.4	1382	3	US-09-023-173-6	Sequence 6, Appl
34	69.2	12.4	1382	3	US-08-046-431A-1	Sequence 1, Appl
35	69.2	12.4	1395	3	US-09-828-592-6	Sequence 6, Appl
36	69.2	12.4	1430	3	US-09-016-434-710	Sequence 710, App
37	69.2	12.4	1467	3	US-09-054-272-3	Sequence 3, Appl
38	69.2	12.4	1525	3	US-10-014-658-16	Sequence 16, Appl
39	69.2	12.4	1599	3	US-09-328-925-43	Sequence 43, Appl
C 40	69	12.4	241	3	US-09-389-681-338	Sequence 338, App
C 41	69	12.4	241	3	US-09-620-405B-338	Sequence 338, App
C 42	69	12.4	241	3	US-09-433-826B-338	Sequence 338, App
C 43	69	12.4	241	3	US-09-604-287A-338	Sequence 338, App
C 44	69	12.4	241	3	US-09-834-759-338	Sequence 338, App
C 45	69	12.4	241	3	US-09-590-751A-338	Sequence 338, App

ALIGNMENTS

RESULT 1
US-08-840-204-1
; Sequence 1, Application US/08840204
; Patent No. 6103498
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: STEFANSSON, STEINGRIMUR P.
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
; TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/840,204
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 30807-20004.00
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 76..1281
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 145
; FEATURE:

NAME/KEY: sig_peptide
LOCATION: 76..144
US-08-840-204-1

Query Match 100.0%; Score 556; DB 3; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2.2e-141; Indels 0; Gaps 0;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACACAGAGCGCATCTTCGTC 60
DB 382 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACACAGAGCGCATCTTCGTC 441

QY 61 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTCAAGCTGTTCGGAGC 120
DB 442 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTCAAGCTGTTCGGAGC 501

QY 121 ACGGTCACGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATCACTGG 180
DB 502 ACGGTCACGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATCACTGG 561

QY 181 GTGAAGACACACACAAAGATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB 562 GTGAAGACACACACAAAGATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 621

QY 241 CTGACACGGCTGTGTGTAATGCTCTTCACTTCAACGGCCAGTGGAAGACTCCCTTC 300
DB 622 CTGACACGGCTGTGTGTAATGCTCTTCACTTCAACGGCCAGTGGAAGACTCCCTTC 681

QY 301 CCGGACTCCAGACCCACCGCGCTCTTCCAAATCAGAGCGGAGCACTGTCTCTGTG 360
DB 682 CCGGACTCCAGACCCACCGCGCTCTTCCAAATCAGAGCGGAGCACTGTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCGGATGCCAT 420
DB 742 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCGGATGCCAT 801

QY 421 TACTACGACATCCTGGAAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 480
DB 802 TACTACGACATCCTGGAAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 861

QY 481 CCTTATGAAAAGAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 540
DB 862 CCTTATGAAAAGAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 921

QY 541 AGCCACTGGAAGGCA 556
DB 922 AGCCACTGGAAGGCA 937

RESULT 2
US-08-840-204-10/c
Sequence 10, Application US/08840204
Patent No. 6103498

GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30807-20004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-840-204-10

Query Match 100.0%; Score 556; DB 3; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2.2e-141; Indels 0; Gaps 0;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACACAGAGCGCATCTTCGTC 60
DB 2495 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACACAGAGCGCATCTTCGTC 2436

QY 61 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTCAAGCTGTTCGGAGC 120
DB 2435 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTCAAGCTGTTCGGAGC 2376

QY 121 ACGGTCACGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATCACTGG 180
DB 2375 ACGGTCACGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATCACTGG 2316

QY 181 GTGAAGACACACACAAAGATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB 2315 GTGAAGACACACACAAAGATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 2256

QY 241 CTGACACGGCTGTGTGTAATGCTCTTCACTTCAACGGGACACCCCTCAGCATGTTTCTGTC 300
DB 2255 CTGACACGGCTGTGTGTAATGCTCTTCACTTCAACGGGACACCCCTCAGCATGTTTCTGTC 2196

QY 301 CCGGACTCCAGACCCACCGCGCTCTTCCAAATCAGAGCGGAGCACTGTCTCTGTG 360
DB 2195 CCGGACTCCAGACCCACCGCGCTCTTCCAAATCAGAGCGGAGCACTGTCTCTGTG 2136

QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCGGATGCCAT 420
DB 2135 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCGGATGCCAT 2076

QY 421 TACTACGACATCCTGGAAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 480
DB 2075 TACTACGACATCCTGGAAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 2016

QY 481 CCTTATGAAAAGAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 540
DB 2015 CCTTATGAAAAGAGTGGCTCTCTGCGCTTACACGGGACACCCCTCAGCATGTTTCTGTC 1956

QY 541 AGCCACTGGAAGGCA 556
DB 1955 AGCCACTGGAAGGCA 1940

RESULT 3
US-09-324-494A-1
Sequence 1, Application US/09324494A
Patent No. 6489143

GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THE
FILE REFERENCE: 30523/167

; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1281)
; OTHER INFORMATION:
US-09-324-494A-1

Query Match 100.0%; Score 556; DB 3; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2.2e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAGGATGAGATCAGACACACAGCGGATCTTCGTC 60
DB 382 AAGGAGCTCATGGGCCATGGAAACAGGATGAGATCAGACACACAGCGGATCTTCGTC 441

QY 61 CAGCGGATCTGAAGTGTGTCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCCGAGC 120
DB 442 CAGCGGATCTGAAGTGTGTCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCCGAGC 501

QY 121 ACGGTCAAGCAAGTGCATTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 180
DB 502 ACGGTCAAGCAAGTGCATTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 561

QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 240
DB 562 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 621

QY 241 CTGACACGGCTGTGTGTAATGTCCTTCAACCGCCAGTGGAAAGACTCCCTTC 300
DB 622 CTGACACGGCTGTGTGTAATGTCCTTCAACCGCCAGTGGAAAGACTCCCTTC 681

QY 301 CCGGACTCCAGCACCCACCGCCCTCTTCCAAATCAGACGGGACACTGTCCTGTG 360
DB 682 CCGGACTCCAGCACCCACCGCCCTCTTCCAAATCAGACGGGACACTGTCCTGTG 741

QY 361 CCATGATGCTCAGACCAACAAAGTTCACATATCTAGTTCACACGCCGCGATGGCCAT 420
DB 742 CCATGATGCTCAGACCAACAAAGTTCACATATCTAGTTCACACGCCGCGATGGCCAT 801

QY 421 TACTAGCATCTCTGAACTGCCCTACCAAGGACACCTCAGCATGTTTCATTTGCTGCC 480
DB 802 TACTAGCATCTCTGAACTGCCCTACCAAGGACACCTCAGCATGTTTCATTTGCTGCC 861

QY 481 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACCAATTCAGTGGCCAGCTCATC 540
DB 862 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACCAATTCAGTGGCCAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
DB 922 AGCCACTGGAAGGCA 937

RESULT 4

US-09-324-494A-10/c
; Sequence 10, Application US/09324494A
; Patent No. 6489143
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, Daniel A
; APPLICANT: STEFANSON, Steingrur P
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
; FILE REFERENCE: 30523/167
; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10

; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-324-494A-10

Query Match 100.0%; Score 556; DB 3; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2.2e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAGGATGAGATCAGACACACAGCGGATCTTCGTC 60
DB 2495 AAGGAGCTCATGGGCCATGGAAACAGGATGAGATCAGACACACAGCGGATCTTCGTC 2436

QY 61 CAGCGGATCTGAAGTGTGTCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCCGAGC 120
DB 2435 CAGCGGATCTGAAGTGTGTCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCCGAGC 2376

QY 121 ACGGTCAAGCAAGTGCATTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 180
DB 2375 ACGGTCAAGCAAGTGCATTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 2316

QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 240
DB 2315 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 2256

QY 241 CTGACACGGCTGTGTGTAATGTCCTTCAACCGCCAGTGGAAAGACTCCCTTC 300
DB 2255 CTGACACGGCTGTGTGTAATGTCCTTCAACCGCCAGTGGAAAGACTCCCTTC 2196

QY 301 CCGGACTCCAGCACCCACCGCCCTCTTCCAAATCAGACGGGACACTGTCCTGTG 360
DB 2195 CCGGACTCCAGCACCCACCGCCCTCTTCCAAATCAGACGGGACACTGTCCTGTG 2136

QY 361 CCATGATGCTCAGACCAACAAAGTTCACATATCTAGTTCACACGCCGCGATGGCCAT 420
DB 2135 CCATGATGCTCAGACCAACAAAGTTCACATATCTAGTTCACACGCCGCGATGGCCAT 2076

QY 421 TACTAGCATCTCTGAACTGCCCTACCAAGGACACCTCAGCATGTTTCATTTGCTGCC 480
DB 2075 TACTAGCATCTCTGAACTGCCCTACCAAGGACACCTCAGCATGTTTCATTTGCTGCC 2016

QY 481 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACCAATTCAGTGGCCAGCTCATC 540
DB 2015 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACCAATTCAGTGGCCAGCTCATC 1956

QY 541 AGCCACTGGAAGGCA 556
DB 1955 AGCCACTGGAAGGCA 1940

RESULT 5

US-09-023-655-1187
; Sequence 1187, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

QY 467 TGTTCATTTGTCGCCCTTATGAAAAAGAGTGCTCTCTCTGCTGCCCTCAACCAACATTCTGA 526
| | | | |
Db 758 TGCTGATTGACTGCCGACTGAGAGTCCACTCGCTGTCTGTCATCATCCACACATCA 817
| | | | |
QY 527 GTGCCAGCTCATCAGCACTGGAAGGCA 556
| | | | |
Db 818 GCACCAAGACCATAGACAGCTGGATGAGCA 847
| | | | |

RESULT 7

5187089-1

; Patent No. 5187089

; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL

; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT

; ELASTASE

; NUMBER OF SEQUENCES: 11

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/542,484

; FILING DATE: 21-JUN-1990

; SEQ ID NO: 1:

; LENGTH: 2029

5187089-1

Query Match 20.5%; Score 114; DB 9; Length 2029;
Best Local Similarity 54.9%; Pred. No. 4e-21;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 110 TGTTCGGAGCAGCGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTTCATCA 169
| | | | |
Db 542 TGTTCAGTGTGAGGTCCGGAATGTGAATTTTCAGGATCCAGCCTCTGCTGTGATTCCA 601
| | | | |
QY 170 TCAATGACTGGTGAAGACACACAAAAGGTATGATCAGCAACTTCTTGGGAAAGGAG 229
| | | | |
Db 602 TCAATGACTGGTGAAGACACAAAAGGTATGATCAGCAACTTCTTGGGAAAGGAG 229
| | | | |
QY 230 CGGTGGA---CCAGCTGACACCGCTGGTGTGATGCTTACTTCAACGGCCAGT 286
| | | | |
Db 662 TTATTGATGGTGTCTCACCAGACTGGTCTCTGTCACGAGTATTTTCAAGGGTCTGT 721
| | | | |
QY 287 GGAAGACTCCCTTCCCGGACTCCAGCACCCAGCGGCTCTTCCCAAAATCAGACGGCA 346
| | | | |
Db 722 GGAATATCAGGTTCACACCGGAGAACACAAAGAAAGCGCACTTTCGGGCGACGGGA 781
| | | | |
QY 347 GCAGTGTCTCTGTCGCCATGATGCTCAGCAACCAAGTTCAACTATCTGATTTCAACA 406
| | | | |
Db 782 AATCCTATCAAGTGCAGTCTCCGCTCTCCGCTGTCGGTGCACAAAGTG 841
| | | | |
QY 407 CGCCGATGCCATTTACTAGGACTCTGGAAGTCCCTTACCGGGGACACCCCTCAGCA 466
| | | | |
Db 842 CCCCCAATGATTATGGTACAACTTCATTGAACTCCCTTACCACGGGGAAGCATCAGCA 901
| | | | |
QY 467 TGTTCATTGCTGCCCTTATGAAAAAGAGTGCTCTCTCTGCCCTCACCACATTTCTGA 526
| | | | |
Db 902 TGCTGATTGCACTGCGGACTGAGAGTCCACTCCGCTGCTGCTGCCATCATCCCAACATCA 961
| | | | |
QY 527 GTGCCAGCTCATCAGCCACTGGAAGGCA 556
| | | | |
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991
| | | | |

RESULT 8

5457090-1

; Patent No. 5457090

; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL

; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS

; NUMBER OF SEQUENCES: 7

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/924,294

; FILING DATE: 03-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 542,484

; FILING DATE: 21-JUN-1990

5457090-1

; SEQ ID NO: 1:
; LENGTH: 2029
5457090-1

Query Match 20.5%; Score 114; DB 9; Length 2029;
Best Local Similarity 54.9%; Pred. No. 4e-21;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 110 TGTTCGGAGCAGCGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTTCATCA 169
| | | | |
Db 542 TGTTCAGTGTGAGGTCCGGAATGTGAATTTTCAGGATCCAGCCTCTGCTGTGATTCCA 601
| | | | |
QY 170 TCAATGACTGGTGAAGACACACAAAAGGTATGATCAGCAACTTCTTGGGAAAGGAG 229
| | | | |
Db 602 TCAATGACTGGTGAAGACACAAAAGGTATGATCAGCAACTTCTTGGGAAAGGAG 229
| | | | |
QY 230 CGGTGGA---CCAGCTGACACCGCTGGTGTGATGCTTACTTCAACGGCCAGT 286
| | | | |
Db 662 TTATTGATGGTGTCTCACCAGACTGGTCTCTGTCACGAGTATTTTCAAGGGTCTGT 721
| | | | |
QY 287 GGAAGACTCCCTTCCCGGACTCCAGCACCCAGCGGCTCTTCCCAAAATCAGACGGCA 346
| | | | |
Db 722 GGAATATCAGGTTCACACCGGAGAACACAAAGAAAGCGCACTTTCGGGCGACGGGA 781
| | | | |
QY 347 GCAGTGTCTCTGTCGCCATGATGCTCAGCAACCAAGTTCAACTATCTGATTTCAACA 406
| | | | |
Db 782 AATCCTATCAAGTGCAGTCTCCGCTCTCCGCTGTCGGTGCACAAAGTG 841
| | | | |
QY 407 CGCCGATGCCATTTACTAGGACTCTGGAAGTCCCTTACCGGGGACACCCCTCAGCA 466
| | | | |
Db 842 CCCCCAATGATTATGGTACAACTTCATTGAACTCCCTTACCACGGGGAAGCATCAGCA 901
| | | | |
QY 467 TGTTCATTGCTGCCCTTATGAAAAAGAGTGCTCTCTCTGCCCTCACCACATTTCTGA 526
| | | | |
Db 902 TGCTGATTGCACTGCGGACTGAGAGTCCACTCCGCTGCTGCTGCCATCATCCCAACATCA 961
| | | | |
QY 527 GTGCCAGCTCATCAGCCACTGGAAGGCA 556
| | | | |
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991
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RESULT 9

5495001-6

; Patent No. 5495001

; APPLICANT: MCGROGAN, MICHAEL P.; SCOTT, RANDY W.; BAKER,

; JOFFRE B.; SIMONSEN, CHRISTIAN C.

; TITLE OF INVENTION: RECOMBINANT PURIFIED PROTEASE NEXIN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/288,596

; FILING DATE: 10-AUG-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 111,111

; FILING DATE: 24-AUG-1993

; APPLICATION NUMBER: 25,450

; FILING DATE: 13-MAR-1987

; APPLICATION NUMBER: 871,501

; FILING DATE: 06-JUN-1986

; APPLICATION NUMBER: 870,232

; FILING DATE: 03-JUN-1986

; SEQ ID NO: 6:

; LENGTH: 2029

5495001-6

Query Match 20.5%; Score 114; DB 9; Length 2029;
Best Local Similarity 54.9%; Pred. No. 4e-21;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 110 TGTTCGGAGCAGCGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTTCATCA 169
| | | | |
Db 542 TGTTCAGTGTGAGGTCCGGAATGTGAATTTTCAGGATCCAGCCTCTGCTGTGATTCCA 601
| | | | |
QY 170 TCAATGACTGGTGAAGACACACAAAAGGTATGATCAGCAACTTCTTGGGAAAGGAG 229
| | | | |

Db 602 TCAATGCTATGGGTTAAATAATGAACACAGGATATGATTGACAATCTGCTGTCCCGAGATC 661
Qy 230 CCGTGGG---CCAGCTGACACCGGCTGGTGTGAATGCCCTCTACTTTCAACGGCCAGT 286
Db 662 TTATTGATGGTGTCTCACCAGACTGGTCTCTGCTCAACGAGTGTATTTCAAGGTCGT 721
Qy 287 GGAAGACTCCCTTCCCGAGCTCCAGACCCACCGCGCTCTTCCACAAATCAGACGGCA 346
Db 722 GGAATACAGGTTCCAAACCGAGAACACAAAGAAACGCACTTTGCTGGCAGCGAGGGA 781
Qy 347 GCACCTGTCTGTGCGCATGATGGCTCAGACCAACAAAGTTCACTATGATGTTCAACA 406
Db 782 AATCCTATCAAGTGGCAATGCTGGCCAGCTCCGCTGCTCGGTGTGGGTGCAAGTG 841
Qy 407 CGCCCGATGGCCATTACTACGACATCTCGGAATCTCCCTACCAAGGAGACACCTTCAGCA 466
Db 842 CCCCAGATGATTATGATGATCAACTTCATTGAATCTCCCTTACCAAGGGAAGCATCAGCA 901
Qy 467 TGTTCAATGCTGCCCTTATGAAAGAGGTGCTCTCTCTGCTCCCTCACCACAACTTCTGA 526
Db 902 TGCTGATTGCACTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 961
Qy 527 GTGCCAGCTATACGCACTCGGAAGGCA 556
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991

RESULT 10
5187089-3
; Patent No. 5187089
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT ELASTASE
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 3
; LENGTH: 2032
5187089-3

Query Match 20.5%; Score 114; DB 9; Length 2032;
Best Local Similarity 54.9%; Pred. No. 4e-21;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

Qy 110 TGTTCGGAGACCGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCA 169
Db 542 TGTTCAGTGTGAGTCCGGAATGTGAATCTTTGAGGATCCAGCCTCTGCTGTGATTCCA 601
Qy 170 TCAATGACTGGGTGAAGACACACACAAAGGTATGATCAGCAACTTGTGTTGGAAAGGAG 229
Db 602 TCAATGCAATGGTTAAACAGAACCAAGGATATGATTGACAATCTGCTGTCCCGAGATC 661
Qy 230 CCGTGGG---CCAGCTGACACCGGCTGGTGTGAATGCCCTCTACTTTCAACGGCCAGT 286
Db 662 TTATTGATGGTGTCTCACCAGACTGGTCTCTGCTCAACGAGTGTATTTCAAGGTCGT 721
Qy 287 GGAAGACTCCCTTCCCGAGCTCCAGACCCACCGCGCTCTTCCACAAATCAGACGGCA 346
Db 722 GGAATACAGGTTCCAAACCGAGAACACAAAGAAACGCACTTTGCTGGCAGCGAGGGA 781
Qy 347 GCACCTGTCTGTGCGCATGATGGCTCAGACCAACAAAGTTCACTATGATGTTCAACA 406
Db 782 AATCCTATCAAGTGGCAATGCTGGCCAGCTCTCGGTGTCCGGTGTGGGTGCAAGTG 841
Qy 407 CGCCCGATGGCCATTACTACGACATCTCGGAATCTCCCTACCAAGGAGACACCTTCAGCA 466
Db 842 CCCCAGATGATTATGATGATCAACTTCATTGAATCTCCCTTACCAAGGGAAGCATCAGCA 901
Qy 467 TGTTCAATGCTGCCCTTATGAAAGAGGTGCTCTCTCTGCTCCCTCACCACAACTTCTGA 526
Db 902 TGCTGATTGCACTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 961

Qy 527 GTGCCAGCTCATCAGCCACTGGAAAGGCA 556
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991

RESULT 11
5457090-3
; Patent No. 5457090
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,294
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 3
; LENGTH: 2032
5457090-3

Query Match 20.5%; Score 114; DB 9; Length 2032;
Best Local Similarity 54.9%; Pred. No. 4e-21;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

Qy 110 TGTTCGGAGACCGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCA 169
Db 542 TGTTCAGTGTGAGTCCGGAATGTGAATCTTTGAGGATCCAGCCTCTGCTGTGATTCCA 601
Qy 170 TCAATGACTGGGTGAAGACACACACAAAGGTATGATCAGCAACTTGTGTTGGAAAGGAG 229
Db 602 TCAATGCAATGGTTAAACAGAACCAAGGATATGATTGACAATCTGCTGTCCCGAGATC 661
Qy 230 CCGTGGG---CCAGCTGACACCGGCTGGTGTGAATGCCCTCTACTTTCAACGGCCAGT 286
Db 662 TTATTGATGGTGTGCTCACCAGACTGGTCTCTGCTCAACGAGTGTATTTCAAGGTCGT 721
Qy 287 GGAAGACTCCCTTCCCGAGCTCCAGACCCACCGCGCTCTTCCACAAATCAGACGGCA 346
Db 722 GGAATACAGGTTCCAAACCGAGAACACAAAGAAACGCACTTTGCTGGCAGCGGAGGA 781
Qy 347 GCACCTGTCTGTGCGCATGATGGCTCAGACCAACAAAGTTCACTATGATGTTCAACA 406
Db 782 AATCCTATCAAGTGGCAATGCTGGCCAGCTCTCGGTGTCCGGTGTGGGTGCAAGTG 841
Qy 407 CGCCCGATGGCCATTACTACGACATCTCGGAATCTCCCTTACCAAGGAGACACCTTCAGCA 466
Db 842 CCCCAGATGATTATGATGATCAACTTCATTGAATCTCCCTTACCAAGGGAAGCATCAGCA 901
Qy 467 TGTTCAATGCTGCCCTTATGAAAGAGGTGCTCTCTGCTCCCTCACCACAACTTCTGA 526
Db 902 TGCTGATTGCACTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 961
Qy 527 GTGCCAGCTCATCAGCCACTGGAAAGGCA 556
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991

RESULT 12
5495001-8
; Patent No. 5495001
; APPLICANT: MCGROGAN, MICHAEL P.; SCOTT, RANDY W.; BAKER,
; JOFFRE B.; SIMONSEN, CHRISTIAN C.
; TITLE OF INVENTION: RECOMBINANT PURIFIED PROTEASE NEXIN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,596
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 111,111
; FILING DATE: 24-AUG-1993
; APPLICATION NUMBER: 25,450

FILING DATE: 13-MAR-1987
APPLICATION NUMBER: 871,501
FILING DATE: 06-JUN-1986
APPLICATION NUMBER: 870,232
FILING DATE: 03-JUN-1986
SEQ ID NO: 8
LENGTH: 2031
5495001-8

Query Match 19.9%; Score 110.8; DB 9; Length 2031;
Best Local Similarity 54.4%; Pred. No. 2.9e-20;
Matches 245; Conservative 0; Mismatches 202; Indels 3; Gaps 1;

QY 110 TGTTCGGAGCAGGTCACAGCAAGTGACATTTTCAGAGGTGGAGAGCCAGATTTCATCA 169
DB 541 TGTTCAGTGTGAGTCCGGAATGTGAATTTTCAGATTCAGGCTTCCTCTGTGATTCGA 600
QY 170 TCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAG 229
DB 601 TCAATGATGGGTGAAGAAATGAACAGGAGATGATGACATCTGCTCTCCAGATC 660
QY 230 CCGTGA---CAGCTGACAGGCTGGTGTGTGAATGCGCTCTACTTCAACGGCCAGT 286
DB 661 TTATTGAGTGTGTGCTCAGCAGACTGGTCTCTGTCACAGCAGTGTATTTCAGGGGTCTGT 720
QY 287 GGAAGACTCCCTTCCCGGACTCCAGCAGCCAGCCGCGCTCTTCCACAATCAGACGGCA 346
DB 721 GGAATACAGGTTCACACCGGAGAACACAAAGAACGCACTTTCTGGGAGCGGAGCGGA 780
QY 347 GCACTCTCTCTGTGCGCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGCTTCACCA 406
DB 781 AATCCTATCAAGTGCCAAAGTGTGCGCCAGCTCTCCGTGTTCGGTGTGGGTGCAAGTG 840
QY 407 CGCCGATGGCCATTAATCAGACATCCTGGAAGTGGTCTTACACAGGGGACACCTCAGCA 466
DB 841 CCCCCAATGATTATGGTACAACTTCATTGAAGTGGCTTACACAGGGGAAAGCATCAGCA 900
QY 467 TGTTCATGCTGCGCTTATGAAGAGAGGTGCTCTCTGCGCTCAGCAATCTCTGA 526
DB 901 TGTGATTGACTGCGGACTGAGAGTCCACTCCGCTGTCTGCCATCATCCACACATCA 960
QY 527 GTGCCAGCTCATCAGCCACTGGAAGGCA 556
DB 961 CCACCAAGACATAGACACTGGATGAGCA 990

RESULT 13
US-07-755-461A-12
; Sequence 12, Application US/07755461A
; Patent No. 5370991
; GENERAL INFORMATION:
; APPLICANT: Remold-O'Donnell, Eileen
; TITLE OF INVENTION: Human Elastase Inhibitor
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eileen Remold-O'Donnell, Ph.D.
; STREET: 197 Clinton Street
; CITY: Brookline
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,461A
; FILING DATE: 19910906
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/314,383
; FILING DATE: 23-FEB-1989

ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0279/7012
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1316 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double standard
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
US-07-755-461A-12

Query Match 12.7%; Score 70.8; DB 2; Length 1316;
Best Local Similarity 51.9%; Pred. No. 2e-09;
Matches 190; Conservative 0; Mismatches 167; Indels 9; Gaps 1;

QY 157 GCAGATTTCATCATCATGCTGGGTGAAGACACACAAAAGGTATGATCAGCAACTTG 216
DB 430 GCAAGGAAGACCATTAACCCAGTGGGTCAAAGCAGACAGACAGAGGAAAAATTCGGGAATG 489
QY 217 CTTGGGAAGAGCCGCTGGACAGCTGACACGGCTGGTGTGTGATGCGCTCTACTTTC 276
DB 490 TTGGTCTCGGGCATGTTGATAACATGACCAAACTTTGTCTAGTAAATGCCATCTATTTC 549
QY 277 AACGGCCAGTGAAGACTCCCTTCCCGACTCCAGCAGCCAGCCGCGCTCTTCCACAA 336
DB 550 AAGGGAACTGAGAGATAAATTCATGAAGAGCCAGACGAAATGACATTCAGATTG 609
QY 337 TCAGACGGCAGCACTGTCTCTGTCGCCATGATGGCTCAGACCAACAAAGTTCAACTATCT 396
DB 610 AATAAGAAAGACAGAAAACTGTGAAATGATGATCAGAGAAAAATTTGCAATATGCG 669
QY 397 GAGTTCCACACCCCGATGGCCATTAAGTACTAGACATCTCTGGAATGCTTACACGGGGAC 456
DB 670 TACAT-----CGAGACCTTAAGTGGCTGTGCTGGAATGCTCTTACCAAGCGGAG 720
QY 457 ACCCTCAGCATGTTCAATGCTGCCCTTATGAAAAAGAGGTGCTCTCTCTGCGCTCACC 516
DB 721 GAGCTCAGCATGTTCACTCTGCTGCGGATGACATTTAGGAGCAGTCCACGGGCTTGAAG 780
QY 517 AACATT 522
DB 781 AAGATT 786

RESULT 14
US-07-679-052A-14
; Sequence 14, Application US/07679052A
; Patent No. 5298400
; GENERAL INFORMATION:
; APPLICANT: WHITEFIELD, Peter L.
; APPLICANT: RICHARDSON, Michael A.
; APPLICANT: BUNN, Clive L.
; TITLE OF INVENTION: RECOMBINANT PRODUCT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,052A
; FILING DATE: 19910506

```

/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 16786/147 CHAC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-9300
/ TELEFAX: (703) 683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1328 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: Other nucleic acid;
/ DESCRIPTION: Synthetic DNA oligonucleotide
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 15..1319
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 15..71
/ OTHER INFORMATION: /product= "Synthetic signal
/ peptide"
/ US-07-679-052A-14

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	Query Match	12.7%	Score 70.6;	DB 2;	Length 1328;
	Best Local Similarity	67.1%;	Pred. N. 2.2e-09;		
	Matches 100;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0;
Qy	151	GAGAGCCGAGATTCATCATCAATGACTGGGTGAAGACACACACAAAGGTATGATCAGC	210		
Db	558	GAAGAAGCTGAAAAAAGAATTAATTCCTGGGTCAAGACTCAACCCAAAGGCAAAATCCCA	617		
Qy	211	AAC TTGCTTGGGAAAGGAGCGGTGGACCGAGCTGACACGGCTGGTGTGCTGGTGAATGCCCTC	270		
Db	618	AAC TTGTTACTGNAGTTCTGTAGATGGGGATACCGATGGTCTGCTGAATGCTGTC	677		
Qy	271	TACTTCAACGGCCAGTGGAAAGACTCCCTTT	299		
Db	678	TACTTCAAGGAAGTGGAAACTCCATT	706		

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RESULT 15
US-07-679-052A-16
; Sequence 16, Application US/07679052A
; Patent No. 5298400
; GENERAL INFORMATION:
; APPLICANT: WHITFELD, Peter L.
; APPLICANT: RICHARDSON, Michael A.
; APPLICANT: BUNN, Clive L.
; TITLE OF INVENTION: RECOMBINANT PRODUCT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,052A
; FILING DATE: 19910506
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768

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; REFERENCE/DOCKET NUMBER: 16786/147 CHAC
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1340 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1331
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 15..86
; OTHER INFORMATION: /product= "a-1-antitrypsin signal"
; US-07-679-052A-16

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	Query Match	12.7%	Score 70.6;	DB 2;	Length 1340;
	Best Local Similarity	67.1%	Pred. No. 2.2e-09;		
	Matches 100;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0;
QY	151	GAGAGGCCAGATTCATCATGACTGGGTGAAGACACACAAAGGATGATGATCAGC	210		
Db	570	GAAGAAGCTAGAAAAAGATTAACTCTGGGTCAAGACTCAACCAAGGCAAAATCCCA	629		
QY	211	AACTTGCTTGGGAAAGAGCGCTGGACAGCTGCACGGCTGGTGTGCTGAATGCCCTC	270		
Db	630	AACTTGTTACTGAAAGTTCTGTAGATGGGGATACCAAGATGGTCTCTGTGAATGCTGTC	689		
QY	271	TACTTCAACGGCCAGTGGAAAGACTCCCTT	299		
Db	690	TACTTCAAGGAAGTGGAAAGCTCCATT	718		

Search completed: March 10, 2006, 01:05:59
Job time : 141.5 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	556	100.0	1209	6	US-10-128-706-17	Sequence 17, Appl
2	556	100.0	1209	9	US-10-512-496-17	Sequence 17, Appl
3	556	100.0	1962	6	US-10-368-995-5	Sequence 5, Appl
4	556	100.0	2177	9	US-10-852-335A-45	Sequence 45, Appl
5	556	100.0	2660	3	US-09-814-353-20146	Sequence 20146, A
6	556	100.0	2870	5	US-10-060-036-131	Sequence 131, Appl
7	556	100.0	2876	6	US-10-128-706-5	Sequence 5, Appl
8	556	100.0	2876	6	US-10-170-385-236	Sequence 236, App
9	556	100.0	2876	6	US-10-259-609-1	Sequence 1, Appl
10	556	100.0	2876	6	US-10-259-609-10	Sequence 10, Appl
11	556	100.0	2876	6	US-10-368-995-3	Sequence 3, Appl
12	556	100.0	2876	7	US-10-197-258-1	Sequence 1, Appl
13	556	100.0	2876	7	US-10-231-956A-419	Sequence 419, App
14	556	100.0	2876	7	US-10-641-643-1187	Sequence 1187, Ap
15	556	100.0	2876	6	US-10-955-157-442	Sequence 442, App
16	556	100.0	2876	9	US-10-512-496-5	Sequence 5, Appl
17	556	100.0	2876	9	US-10-508-406-1	Sequence 1, Appl
18	556	100.0	2876	9	US-10-631-467-399	Sequence 399, App
19	556	100.0	2937	8	US-10-775-169-229	Sequence 229, App
20	556	100.0	3171	6	US-10-240-965-160	Sequence 160, App
21	556	100.0	3172	5	US-10-044-090-842	Sequence 842, App
22	556	100.0	3172	5	US-10-084-817-6	Sequence 6, Appl
23	554.4	99.7	1482	5	US-10-193-656-9	Sequence 9, Appl

QY 361 CCCATGATGGCTCAGACCAAGATTCACTACTACTAGATTACACACGCCGATGGCCAT 420
Db 667 CCCATGATGGCTCAGACCAAGATTCACTACTACTAGATTACACACGCCGATGGCCAT 726
QY 421 TACTACGACATCCTGGAACCTGACACAGGGGACACCTCAGCATGTTCAATTCCTGCC 480
Db 727 TACTACGACATCCTGGAACCTGACACAGGGGACACCTCAGCATGTTCAATTCCTGCC 786
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCTTCCCTTACCAACATTTCTGAGTGCCAGCTCATC 540
Db 787 CTTTATGAAAAGAGTGCTCTCTCTGCTTCCCTTACCAACATTTCTGAGTGCCAGCTCATC 846
QY 541 AGCCACTGGAAGGCA 556
Db 847 AGCCACTGGAAGGCA 862

RESULT 2

US-10-512-496-17
; Sequence 17, Application US/10512496
; Publication No. US20050148527A1
; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
; FILE REFERENCE: 0575/66601-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/512,496
; CURRENT FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-512-496-17

Query Match 100.0%; Score 556; DB 9; Length 1209;
Best Local Similarity 100.0%; Pred. No. 3.5e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCCATGGAAACAGGATGAGATCAGCACACAGCGCATCTTCGTC 60
Db 307 AAGGAGCTCATGGGCGCCATGGAAACAGGATGAGATCAGCACACAGCGCATCTTCGTC 366
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCTTCTTCAGGCTGTTCGGAGC 120
Db 367 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCTTCTTCAGGCTGTTCGGAGC 426
QY 121 ACGGTCAAGCAAGTGGAATTTTTCAGAGTGGAGAGGCGAGATTCATCAATGACTGG 180
Db 427 ACGGTCAAGCAAGTGGAATTTTTCAGAGTGGAGAGGCGAGATTCATCAATGACTGG 486
QY 181 GTGAGACACACACAAAAGGTATGATCAGCACTTGTGGAAAGGAGCGTGGACCG 240
Db 487 GTGAGACACACACAAAAGGTATGATCAGCACTTGTGGAAAGGAGCGTGGACCG 546
QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 300
Db 547 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 606
QY 301 CCCGACTCAGACACCGCCGCTCTTTCACAAATCAGAGCGGAGCACTGTCTCTGTG 360
Db 607 CCCGACTCAGACACCGCCGCTCTTTCACAAATCAGAGCGGAGCACTGTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAAGATTCACTACTACTAGATTACACACGCCGATGGCCAT 420
Db 667 CCCATGATGGCTCAGACCAAGATTCACTACTACTAGATTACACACGCCGATGGCCAT 726
QY 421 TACTACGACATCCTGGAACCTGACACAGGGGACACCTCAGCATGTTCAATTCCTGCC 480
Db 727 TACTACGACATCCTGGAACCTGACACAGGGGACACCTCAGCATGTTCAATTCCTGCC 786
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCTTCCCTTACCAACATTTCTGAGTGCCAGCTCATC 540

Db 787 CTTTATGAAAAGAGTGCTCTCTCTGCTTCCCTTACCAACATTTCTGAGTGCCAGCTCATC 846
QY 541 AGCCACTGGAAGGCA 556
Db 847 AGCCACTGGAAGGCA 862

RESULT 3

US-10-368-995-5
; Sequence 5, Application US/10368995
; Publication No. US20030217371A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Eren, Mesut
; APPLICANT: Declerk, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON-
; TITLE OF INVENTION: ANIMAL
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1161)
; OTHER INFORMATION:
US-10-368-995-5

Query Match 100.0%; Score 556; DB 6; Length 1962;
Best Local Similarity 100.0%; Pred. No. 4.1e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCCATGGAAACAGGATGAGATCAGCACACAGCGCATCTTCGTC 60
Db 259 AAGGAGCTCATGGGCGCCATGGAAACAGGATGAGATCAGCACACAGCGCATCTTCGTC 318
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCTTCTTCAGGCTGTTCGGAGC 120
Db 319 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCTTCTTCAGGCTGTTCGGAGC 378
QY 121 ACGGTCAAGCAAGTGGAATTTTTCAGAGTGGAGAGGCGAGATTCATCAATGACTGG 180
Db 379 ACGGTCAAGCAAGTGGAATTTTTCAGAGTGGAGAGGCGAGATTCATCAATGACTGG 438
QY 181 GTGAGACACACACAAAAGGTATGATCAGCACTTGTGGAAAGGAGCGTGGACCG 240
Db 439 GTGAGACACACACAAAAGGTATGATCAGCACTTGTGGAAAGGAGCGTGGACCG 498
QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 300
Db 499 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 558
QY 301 CCCGACTCAGACACCGCCGCTCTTTCACAAATCAGAGCGGAGCACTGTCTCTGTG 360
Db 559 CCCGACTCAGACACCGCCGCTCTTTCACAAATCAGAGCGGAGCACTGTCTCTGTG 618
QY 361 CCCATGATGGCTCAGACCAAGATTCACTACTACTAGATTACACACGCCGATGGCCAT 420
Db 619 CCCATGATGGCTCAGACCAAGATTCACTACTACTAGATTACACACGCCGATGGCCAT 678
QY 421 TACTACGACATCCTGGAACCTGACACAGGGGACACCTCAGCATGTTCAATTCCTGCC 480
Db 679 TACTACGACATCCTGGAACCTGACACAGGGGACACCTCAGCATGTTCAATTCCTGCC 738
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCTTCCCTTACCAACATTTCTGAGTGCCAGCTCATC 540
Db 739 CTTTATGAAAAGAGTGCTCTCTCTGCTTCCCTTACCAACATTTCTGAGTGCCAGCTCATC 798
QY 541 AGCCACTGGAAGGCA 556

Db 799 AGCCACTGGAAAGGCA 814
RESULT 4
US-10-852-335A-45
; Sequence 45, Application US/10852335A
; Publication No. US20050112129A1
; GENERAL INFORMATION:
; APPLICANT: HEIDI S. PHILLIPS
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and Treatment of Tumors of Glial Origin
; FILE REFERENCE: P5103R1-US
; CURRENT APPLICATION NUMBER: US/10/852.335A
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/548,299
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/473,238
; PRIOR FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 45
; LENGTH: 2177
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-335A-45
Query Match 100.0%; Score 556; DB 9; Length 2177;
Best Local Similarity 100.0%; Pred. No. 4.3e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCCATCGAACAGGATGAGATCAGCACCACAGACGGAGTCTCGTC 60
Db 414 AAGGAGCTCATGGGCCATCGAACAGGATGAGATCAGCACCACAGACGGAGTCTCGTC 473
QY 61 CAGCGGGATCTGAAGCTGTGTCAGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGGAGC 120
Db 474 CAGCGGGATCTGAAGCTGTGTCAGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGGAGC 533
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 180
Db 534 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 593
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGCTGGACCAG 240
Db 594 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGCTGGACCAG 653
QY 241 CTGACACGGCTGTGTGTGAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 654 CTGACACGGCTGTGTGTGAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 713
QY 301 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTCTGTG 360
Db 714 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTCTGTG 773
QY 361 CCCATGATGCTCAGACCAAGTTCACTACTAGTTTACACGGCCGATGGCCAT 420
Db 774 CCCATGATGCTCAGACCAAGTTCACTACTAGTTTACACGGCCGATGGCCAT 833
QY 421 TACTAGACATCTGGAAGTGCCTTACCAGGGGACACCTCAGCATGTTTCATTGCTGCC 480
Db 834 TACTAGACATCTGGAAGTGCCTTACCAGGGGACACCTCAGCATGTTTCATTGCTGCC 893
QY 481 CCTTATGAAAAGAGGTGCTCTCTGTGCCCTCACCACCAATTCAGATGCCAGCTCATC 540
Db 894 CCTTATGAAAAGAGGTGCTCTCTGTGCCCTCACCACCAATTCAGATGCCAGCTCATC 953
QY 541 AGCCACTGGAAAGGCA 556
Db 954 AGCCACTGGAAAGGCA 969
RESULT 5
US-09-814-353-20146

; Sequence 20146, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20146
; LENGTH: 2660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-20146
Query Match 100.0%; Score 556; DB 3; Length 2660;
Best Local Similarity 100.0%; Pred. No. 4.6e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCCATCGAACAGGATGAGATCAGCACCACAGACGGAGTCTCGTC 60
Db 452 AAGGAGCTCATGGGCCATCGAACAGGATGAGATCAGCACCACAGACGGAGTCTCGTC 511
QY 61 CAGCGGGATCTGAAGCTGTGTCAGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGGAGC 120
Db 512 CAGCGGGATCTGAAGCTGTGTCAGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGGAGC 571
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 180
Db 572 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 631
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGCTGGACCAG 240
Db 632 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGCTGGACCAG 691
QY 241 CTGACACGGCTGTGTGTGAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 692 CTGACACGGCTGTGTGTGAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 751
QY 301 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTCTGTG 360
Db 752 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTCTGTG 811
QY 361 CCCATGATGCTCAGACCAAGTTCACTACTAGTTTCAACCGCCGATGGCCAT 420
Db 812 CCCATGATGCTCAGACCAAGTTCACTACTAGTTTCAACCGCCGATGGCCAT 871
QY 421 TACTAGACATCTGGAAGTGCCTTACCAGGGGACACCTCAGCATGTTTCATTGCTGCC 480
Db 872 TACTAGACATCTGGAAGTGCCTTACCAGGGGACACCTCAGCATGTTTCATTGCTGCC 931
QY 481 CCTTATGAAAAGAGGTGCTCTCTGTGCCCTCACCACCAATTCAGATGCCAGCTCATC 540
Db 932 CCTTATGAAAAGAGGTGCTCTCTGTGCCCTCACCACCAATTCAGATGCCAGCTCATC 991
QY 541 AGCCACTGGAAAGGCA 556

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DB 992 AGCCACTGGAAGGCA 1007
|||||
RESULT 6
US-10-060-036-131
; Sequence 131, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 2870
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-131

Query Match 100.0%; Score 556; DB 5; Length 2870;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGACACACAGAGCGGATCTTCGTC 60
DB 376 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGACACACAGAGCGGATCTTCGTC 435
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCCGGAGC 120
DB 436 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCCGGAGC 495
QY 121 AGGTCACAGCAAGTGACATTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 180
DB 496 AGGTCACAGCAAGTGACATTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 555
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB 556 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 615
QY 241 CTGACACGGCTGGTGGTGAATGCGCTTACTTCAACGGCCAGTGGAGAGACTCCCTTC 300
DB 616 CTGACACGGCTGGTGGTGAATGCGCTTACTTCAACGGCCAGTGGAGAGACTCCCTTC 675
QY 301 CCGGACTCAGACACCCAGCGCGCTTCTTCCAAATCAGAGGAGCACTGTCTCTGTG 360
DB 676 CCGGACTCAGACACCCAGCGCGCTTCTTCCAAATCAGAGGAGCACTGTCTCTGTG 735
QY 361 CCCATGATGGCTCAGACCAACAGTTCAACTATCTGAGTTCAACACCGCCGATGGCCAT 420
DB 736 CCCATGATGGCTCAGACCAACAGTTCAACTATCTGAGTTCAACACCGCCGATGGCCAT 795
QY 421 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGATGTTCAATGCTGCC 480
DB 796 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGATGTTCAATGCTGCC 855
QY 481 CTTTATGAAAAAGAGTGGCTCTCTGTGCCCTCAGCAACATTTCTGAGTGGCCAGTCTATC 540
DB 856 CTTTATGAAAAAGAGTGGCTCTCTGTGCCCTCAGCAACATTTCTGAGTGGCCAGTCTATC 915
QY 541 AGCCACTGGAAGGCA 556
DB 916 AGCCACTGGAAGGCA 931

RESULT 7
US-10-128-706-5
; Sequence 5, Application US/10128706
; Publication No. US20030199463A1
; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; FILE REFERENCE: 0575/66601
; CURRENT APPLICATION NUMBER: US/10/128,706
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-128-706-5

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGACACACAGAGCGGATCTTCGTC 60
DB 382 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGACACACAGAGCGGATCTTCGTC 441
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
DB 442 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 501
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 180
DB 502 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 561
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB 562 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGTGGGAAAGGAGCCGTGGACCA 621
QY 241 CTGACACGGCTGGTGGTGAATGCGCTTACTTCAACGGCCAGTGGAGAGACTCCCTTC 300
DB 622 CTGACACGGCTGGTGGTGAATGCGCTTACTTCAACGGCCAGTGGAGAGACTCCCTTC 681
QY 301 CCGGACTCAGACACCCAGCGCGCTTCTTCCAAATCAGAGGAGCACTGTCTCTGTG 360
DB 682 CCGGACTCAGACACCCAGCGCGCTTCTTCCAAATCAGAGGAGCACTGTCTCTGTG 741
QY 361 CCGATGATGGCTCAGACCAACAGTTCAATATCTGAGTTCAACACCGCCGATGGCCAT 420
DB 742 CCGATGATGGCTCAGACCAACAGTTCAATATCTGAGTTCAACACCGCCGATGGCCAT 801
QY 421 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGATGTTCAATGCTGCC 480
DB 802 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGATGTTCAATGCTGCC 861
QY 481 CTTTATGAAAAAGAGTGGCTCTCTGTGCCCTCAGCAACATTTCTGAGTGGCCAGTCTATC 540
DB 862 CTTTATGAAAAAGAGTGGCTCTCTGTGCCCTCAGCAACATTTCTGAGTGGCCAGTCTATC 921
QY 541 AGCCACTGGAAGGCA 556
DB 922 AGCCACTGGAAGGCA 937

RESULT 8
US-10-170-385-236
; Sequence 236, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
```

APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-05-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 236
LENGTH: 2876
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-170-385-236

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGACCCACAGACGGGATCTTCGTC 60
DB 382 AAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGACCCACAGACGGGATCTTCGTC 441
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
DB 442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 501
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 180
DB 502 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 561
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTCTTGGGAAAGAGCGGTGGACCG 240
DB 562 GTGAAGACACACAAAGGTATGATCAGCAACTTCTTGGGAAAGAGCGGTGGACCG 621
QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
DB 622 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681
QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 360
DB 682 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 741
QY 361 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTTACCGCCCGATGGCCAT 420
DB 742 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTTACCGCCCGATGGCCAT 801
QY 421 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGCTGCC 480
DB 802 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGCTGCC 861
QY 481 CTTATGAAAAAGAGTGCTCTCTGCGCCCTCACCAATTCAGTGCCCGAGCTCATC 540
DB 862 CTTATGAAAAAGAGTGCTCTCTGCGCCCTCACCAATTCAGTGCCCGAGCTCATC 921
QY 541 AGCCACTGGAAAGGCA 556
DB 922 AGCCACTGGAAAGGCA 937

RESULT 9
US-10-259-609-1
Sequence 1, Application US/10259609
Publication No. US20030216321A1
GENERAL INFORMATION:
APPLICANT: LAWRENCE, Daniel A
APPLICANT: STEFANSSON, Steingrur P

TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THE
FILE REFERENCE: 30523/167
CURRENT APPLICATION NUMBER: US/10/259,609
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/324,494A
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2876
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (76)..(1281)
OTHER INFORMATION:
US-10-259-609-1

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGACCCACAGACGGGATCTTCGTC 60
DB 382 AAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGACCCACAGACGGGATCTTCGTC 441
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
DB 442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 501
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 180
DB 502 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 561
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTCTTGGGAAAGAGCGGTGGACCG 240
DB 562 GTGAAGACACACAAAGGTATGATCAGCAACTTCTTGGGAAAGAGCGGTGGACCG 621
QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
DB 622 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681
QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 360
DB 682 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 741
QY 361 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTTACCGCCCGATGGCCAT 420
DB 742 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTTACCGCCCGATGGCCAT 801
QY 421 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGCTGCC 480
DB 802 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGCTGCC 861
QY 481 CTTATGAAAAAGAGTGCTCTCTGCGCCCTCACCAATTCAGTGCCCGAGCTCATC 540
DB 862 CTTATGAAAAAGAGTGCTCTCTGCGCCCTCACCAATTCAGTGCCCGAGCTCATC 921
QY 541 AGCCACTGGAAAGGCA 556
DB 922 AGCCACTGGAAAGGCA 937

RESULT 10
US-10-259-609-10/c
Sequence 10, Application US/10259609
Publication No. US20030216321A1
GENERAL INFORMATION:
APPLICANT: LAWRENCE, Daniel A
APPLICANT: STEFANSSON, Steingrur P
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THE
FILE REFERENCE: 30523/167
CURRENT APPLICATION NUMBER: US/10/259,609

;/ CURRENT FILING DATE: 2002-09-30
;/ PRIOR APPLICATION NUMBER: US/09/324,494A
;/ PRIOR FILING DATE: 1999-06-02
;/ NUMBER OF SEQ ID NOS: 29
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 10
;/ LENGTH: 2876
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
US-10-259-609-10

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCATGGACCAAGGATGATCAGCACACAGCGCGATCTCGTC 60
Db AAGGAGCTCATGGGGCCATGGACCAAGGATGATCAGCACACAGCGCGATCTCGTC 2436
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTTCATGCCCACTTCTTCAGGGCTGTTCCGGAGC 120
Db CAGCGGGATCTGAAGCTGGTCCAGGGCTTTCATGCCCACTTCTTCAGGGCTGTTCCGGAGC 2376
QY 121 AGGTCACGAGATGAGCTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 180
Db AGGTCACGAGATGAGCTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 2316
QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
Db GTGAAGACACACACAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 2256
QY 241 CTGACACGGCTGGTGGTGAATGCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db CTGACACGGCTGGTGGTGAATGCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 2196
QY 301 CCGGACTCCAGCACCCACCGCGCTTTCCTTCCAAATCAGAGGAGCACTGTCTCTGTG 360
Db CCGGACTCCAGCACCCACCGCGCTTTCCTTCCAAATCAGAGGAGCACTGTCTCTGTG 2136
QY 361 CCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTCACACGCCCGATGCCAT 420
Db CCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTCACACGCCCGATGCCAT 2076
QY 421 TACTAGCATCTCTGAACTGGCTTACCAACGGGACACCCCTCAGCATGTTCTGTC 480
Db TACTAGCATCTCTGAACTGGCTTACCAACGGGACACCCCTCAGCATGTTCTGTC 2016
QY 481 CTTATGAAAAAGAGTGCTCTCTGCTCCCTACCAACATTCAGTGCCCGAGCTCATC 540
Db CTTATGAAAAAGAGTGCTCTCTGCTCCCTACCAACATTCAGTGCCCGAGCTCATC 1956
QY 541 AGCCACTGGAAGGCA 556
Db AGCCACTGGAAGGCA 1940

RESULT 11
US-10-368-995-3
;/ Sequence 3, Application US/10368995
;/ Publication No. US20030217371A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Vaughan, Douglas E.
;/ APPLICANT: Eren, Mesut
;/ APPLICANT: Declerk, Paul J.
;/ TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
;/ FILE REFERENCE: 1242/43
;/ CURRENT APPLICATION NUMBER: US/10/368,995
;/ CURRENT FILING DATE: 2003-02-19
;/ NUMBER OF SEQ ID NOS: 16
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 3
;/ LENGTH: 2876

;/ TYPE: DNA
;/ ORGANISM: Human
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: (76)..(1284)
;/ OTHER INFORMATION:
US-10-368-995-3

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCATGGACCAAGGATGATCAGCACACAGCGCGATCTTCGTC 60
Db AAGGAGCTCATGGGGCCATGGACCAAGGATGATCAGCACACAGCGCGATCTTCGTC 441
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTTCATGCCCACTTCTTCAGGGCTGTTCCGGAGC 120
Db CAGCGGGATCTGAAGCTGGTCCAGGGCTTTCATGCCCACTTCTTCAGGGCTGTTCCGGAGC 501
QY 121 AGGTCACGAGATGAGCTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 180
Db AGGTCACGAGATGAGCTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 561
QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
Db GTGAAGACACACACAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 621
QY 241 CTGACACGGCTGGTGGTGAATGCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db CTGACACGGCTGGTGGTGAATGCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 681
QY 301 CCGGACTCCAGCACCCACCGCGCTTTCCTTCCAAATCAGAGGAGCACTGTCTCTGTG 360
Db CCGGACTCCAGCACCCACCGCGCTTTCCTTCCAAATCAGAGGAGCACTGTCTCTGTG 741
QY 361 CCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTCACACGCCCGATGCCAT 420
Db CCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTCACACGCCCGATGCCAT 801
QY 421 TACTAGCATCTCTGAACTGGCTTACCAACGGGACACCCCTCAGCATGTTCTGTC 480
Db TACTAGCATCTCTGAACTGGCTTACCAACGGGACACCCCTCAGCATGTTCTGTC 861
QY 481 CTTATGAAAAAGAGTGCTCTCTGCTCCCTACCAACATTCAGTGCCCGAGCTCATC 540
Db CTTATGAAAAAGAGTGCTCTCTGCTCCCTACCAACATTCAGTGCCCGAGCTCATC 921
QY 541 AGCCACTGGAAGGCA 556
Db AGCCACTGGAAGGCA 937

RESULT 12
US-10-197-258-1
;/ Sequence 1, Application US/10197258
;/ Publication No. US20040014190A1
;/ GENERAL INFORMATION:
;/ APPLICANT: LAWRENCE, DANIEL A.
;/ APPLICANT: GORLATOVA, NATALIA
;/ APPLICANT: CRANDALL, DAVID L.
;/ TITLE OF INVENTION: MUTANT PROTEINASE-INHIBITORS AND USES THEREOF
;/ FILE REFERENCE: 030523-0187
;/ CURRENT APPLICATION NUMBER: US/10/197,258
;/ CURRENT FILING DATE: 2002-07-18
;/ NUMBER OF SEQ ID NOS: 12
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 1
;/ LENGTH: 2876
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: CDS


```
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1187:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2876 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g189541
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1187 :
US-10-641-643-1187

Query Match          100.0%; Score 556; DB 7; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGCACACAGACCGGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGCACACAGACCGGATCTTCGTC 441

QY 61 CAGCGGGATCTGAAGTGGTCCAGGGCTTCATGCCCACTTCTTCAAGGCTGTTCGGAGC 120
Db 442 CAGCGGGATCTGAAGTGGTCCAGGGCTTCATGCCCACTTCTTCAAGGCTGTTCGGAGC 501

QY 121 ACGGTCAAGCAAGTGGATTTTTCAGAGTGGAGAGCCAGATTTCATCAATCAATGCTGG 180
Db 502 ACGGTCAAGCAAGTGGATTTTTCAGAGTGGAGAGCCAGATTTCATCAATCAATGCTGG 561

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 240
Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 621

QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGGAAGACTCCCTTC 300
Db 622 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGGAAGACTCCCTTC 681

QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGGAGCCGTGGACCG 360
Db 682 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGGAGCCGTGGACCG 741

QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCAACCGCCGATGGCCAT 420
Db 742 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCAACCGCCGATGGCCAT 801

QY 421 TACTACGACATCTTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTCAATTGCTGCC 480
Db 802 TACTACGACATCTTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTCAATTGCTGCC 861

QY 481 CTTTATGAAAAAGAGTGGCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 540
Db 862 CTTTATGAAAAAGAGTGGCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
Db 922 AGCCACTGGAAGGCA 937
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RESULT 15
US-10-956-157-442
/ Sequence 442, Application US/10956157
/ Publication No. US20050118625A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
/ TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
/ FILE REFERENCE: 031896-043000 (AM 101081)
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/ CURRENT APPLICATION NUMBER: US/10/956,157
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 319805
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 442
/ LENGTH: 2876
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-956-157-442

Query Match          100.0%; Score 556; DB 9; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGCACACAGACCGGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGCGCATGGAACAGGATGAGATCAGCACACAGACCGGATCTTCGTC 441

QY 61 CAGCGGGATCTGAAGTGGTCCAGGGCTTCATGCCCACTTCTTCAAGGCTGTTCGGAGC 120
Db 442 CAGCGGGATCTGAAGTGGTCCAGGGCTTCATGCCCACTTCTTCAAGGCTGTTCGGAGC 501

QY 121 ACGGTCAAGCAAGTGGATTTTTCAGAGTGGAGAGCCAGATTTCATCAATCAATGCTGG 180
Db 502 ACGGTCAAGCAAGTGGATTTTTCAGAGTGGAGAGCCAGATTTCATCAATCAATGCTGG 561

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 240
Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 621

QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGGAAGACTCCCTTC 300
Db 622 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGGAAGACTCCCTTC 681

QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGGAGCCGTGGACCG 360
Db 682 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGGAGCCGTGGACCG 741

QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCAACCGCCGATGGCCAT 420
Db 742 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCAACCGCCGATGGCCAT 801

QY 421 TACTACGACATCTTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTCAATTGCTGCC 480
Db 802 TACTACGACATCTTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTCAATTGCTGCC 861

QY 481 CTTTATGAAAAAGAGTGGCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 540
Db 862 CTTTATGAAAAAGAGTGGCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
Db 922 AGCCACTGGAAGGCA 937
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Search completed: March 10, 2006, 01:43:32
Job time : 675 secs

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2006, 01:21:06 ; Search time 322 Seconds
(without alignments)

3984.028 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793

Perfect score: 556

Sequence: 1 aaggactcagggccatg.....catcagccactggaaggca 556

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
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- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	1209	8	US-10-821-234-729
2	556	100.0	2522	12	US-11-094-519A-11
3	556	100.0	2876	12	US-11-091-883-114
4	556	100.0	2937	8	US-10-775-169-229
5	556	100.0	3273	12	US-11-091-883-113
6	479	86.2	2438	12	US-11-094-519A-10
7	421.6	75.8	3053	12	US-11-136-527-3753
8	166.8	30.0	1404	8	US-10-750-185-46781
9	166.8	30.0	1404	8	US-10-750-623-46781
10	165.6	29.8	14302	12	US-11-136-527-3649
11	114	20.5	1191	9	US-11-245-147-95
12	114	20.5	1197	8	US-10-821-234-636
13	114	20.5	2129	12	US-11-186-284-184
14	98.4	17.0	1212	9	US-11-245-147-20
15	94.6	17.0	1963	12	US-11-136-527-1947
16	71.8	12.9	1398	7	US-10-959-322-2
17	71.8	12.9	1736	8	US-10-995-561-409
18	71.8	12.9	1911	8	US-10-995-561-410
19	70.6	12.7	1400	12	US-11-136-527-6043
20	70.6	12.7	1900	8	US-10-775-169-49

21	70.6	12.7	1900	12	US-11-091-883-135	Sequence 135, App
22	69.8	12.6	2081	12	US-11-128-061-1036	Sequence 1036, App
23	69.8	12.6	2081	12	US-11-128-049-1036	Sequence 1036, App
24	69.2	12.4	1299	7	US-10-959-322-40	Sequence 40, Appl
25	69.2	12.4	1395	7	US-10-959-309-18	Sequence 18, Appl
26	69.2	12.4	1395	7	US-10-959-322-1	Sequence 1, Appl
27	69.2	12.4	1599	9	US-11-129-861-43	Sequence 43, Appl
28	69	12.4	1918	8	US-10-821-234-48	Sequence 48, Appl
29	67	12.1	257	12	US-11-128-061-404	Sequence 404, App
30	67	12.1	257	12	US-11-128-061-404	Sequence 404, App
31	67	12.1	257	12	US-11-128-049-404	Sequence 404, App
32	67	12.1	257	12	US-11-128-049-404	Sequence 404, App
33	65	11.7	1378	12	US-11-128-061-873	Sequence 873, App
34	65	11.7	1378	12	US-11-128-049-873	Sequence 873, App
35	64.8	11.7	1370	9	US-11-048-774-12	Sequence 12, Appl
36	64.8	11.7	1371	9	US-11-048-774-1	Sequence 1, Appl
37	64.4	11.6	1943	12	US-11-136-527-2587	Sequence 2587, App
38	60.2	10.8	201	8	US-10-995-561-10853	Sequence 10853, A
39	60.2	10.8	201	8	US-10-995-561-10866	Sequence 10866, A
40	59.4	10.7	1466	8	US-10-276-233A-14	Sequence 14, Appl
41	59.4	10.7	2480	9	US-11-072-512-1410	Sequence 1410, App
42	59	10.6	1606	8	US-10-995-561-278	Sequence 278, App
43	59	10.6	1655	8	US-10-995-561-277	Sequence 277, App
44	59	10.6	2480	8	US-10-995-561-276	Sequence 276, App
45	57.6	10.4	1690	12	US-11-136-527-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-10-821-234-729

; Sequence 729, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt_seq_genes Version 1.0

; SEQ ID NO 729

; LENGTH: 1209

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-821-234-729

Query Match	100.0%	Score 556;	DB 8;	Length 1209;
Best Local Similarity	100.0%;	Pred. No. 6.8e-150;		
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGGAGCTCATGGGCGCATGGAAAGGATGAGATCAGACACACGCGATCTTCGTC	60	
Db	307	AAGGAGCTCATGGGCGCATGGAAAGGATGAGATCAGACACACGCGATCTTCGTC	366	
QY	61	CAGCGGAGTCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCCTTCAGGGTGTTCGGGAGC	120	
Db	367	CAGCGGAGTCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCCTTCAGGGTGTTCGGGAGC	426	
QY	121	ACGGTCAAGCAAGTGAAGCTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG	180	
Db	427	ACGGTCAAGCAAGTGAAGCTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG	486	
QY	181	GTGAACACACACACAAAGGATGATCAGCACTTCCTGGGAAGGAGCCGTGGACCAG	240	
Db	487	GTGAACACACACACAAAGGATGATCAGCACTTCCTGGGAAGGAGCCGTGGACCAG	546	

QY 241 CTGACAGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
| | | | |
Db 547 CTGACAGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 606
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QY 301 CCGGACTCAGACACCACCGCGCTCTTCCAAATCAGCGGAGCACTGTCTCTGTG 360
| | | | |
Db 607 CCGGACTCAGACACCACCGCGCTCTTCCAAATCAGCGGAGCACTGTCTCTGTG 666
| | | | |
QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGTAGTTTCAACACGCCCGATGGCCAT 420
| | | | |
Db 667 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGTAGTTTCAACACGCCCGATGGCCAT 726
| | | | |
QY 421 TACTAGACATCTGGAATCGCCCTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 480
| | | | |
Db 727 TACTAGACATCTGGAATCGCCCTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 786
| | | | |
QY 481 CTTTATGAAAAAGAGTGGCTCTCTGCGCTTCAACAACTTCTGAGTCCCGAGCTCATC 540
| | | | |
Db 787 CTTTATGAAAAAGAGTGGCTCTCTGCGCTTCAACAACTTCTGAGTCCCGAGCTCATC 846
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QY 541 AGCCACTGGAAGGCA 556
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Db 847 AGCCACTGGAAGGCA 862
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RESULT 2

US-11-094-519A-11

; Sequence 11, Application US/11094519A

; Publication No. US20050281810A1

; GENERAL INFORMATION:

; APPLICANT: BERNSTEIN, Jeanne

; APPLICANT: LEVINE, Zurit

; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

; FILE REFERENCE: 2786-0140P

; CURRENT APPLICATION NUMBER: US/11/094,519A

; CURRENT FILING DATE: 2005-03-31

; PRIOR APPLICATION NUMBER: US/09/695,293

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: IL 132558

; PRIOR FILING DATE: 1999-10-25

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 2522

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-094-519A-11

Query Match 100.0%; Score 556; DB 12; Length 2522;
Best Local Similarity 100.0%; Pred. No. 8.3e-150;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAAACAAAGATGAGATCAGACACACAGACCGCATCTTCGTC 60
| | | | |
Db 454 AAGGAGCTCATGGGCGCATGGAAACAAAGATGAGATCAGACACACAGACCGCATCTTCGTC 513
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QY 61 CAGCGGATCTAGCTGTGTCCAGGCTTCATGCCCTTCTTCCAGGCTGTTCGGAGC 120
| | | | |
Db 514 CAGCGGATCTAGCTGTGTCCAGGCTTCATGCCCTTCTTCCAGGCTGTTCGGAGC 573
| | | | |
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCATCAATGACTGG 180
| | | | |
Db 574 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCATCAATGACTGG 633
| | | | |
QY 181 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCCAG 240
| | | | |
Db 634 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGTGGGAAAGGAGCCGTGGACCCAG 693
| | | | |
QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAGACTCCCTTC 300
| | | | |
Db 694 CTGACACGGCTGGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAGACTCCCTTC 753
| | | | |
QY 301 CCGGACTCAGACACCACCGCGCTCTTCCAAATCAGCGGAGCACTGTCTCTGTG 360
| | | | |

Db 754 CCGGACTCAGACACCACCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 813
| | | | |
QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGTAGTTTCAACACGCCCGATGGCCAT 420
| | | | |
Db 814 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGTAGTTTCAACACGCCCGATGGCCAT 873
| | | | |
QY 421 TACTAGACATCTCGAAATCGCCCTTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 480
| | | | |
Db 874 TACTAGACATCTCGAAATCGCCCTTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 933
| | | | |
QY 481 CTTTATGAAAAAGAGTGGCTCTCTGCGCTTCAACAACTTCTGAGTCCCGAGCTCATC 540
| | | | |
Db 934 CTTTATGAAAAAGAGTGGCTCTCTGCGCTTCAACAACTTCTGAGTCCCGAGCTCATC 993
| | | | |
QY 541 AGCCACTGGAAGGCA 556
| | | | |
Db 994 AGCCACTGGAAGGCA 1009
| | | | |

RESULT 3

US-11-091-883-114

; Sequence 114, Application US/11091883

; Publication No. US20060024693A1

; GENERAL INFORMATION:

; APPLICANT: CIBELLI, JOSE

; APPLICANT: PERNANDEZ, EMILIO O.

; APPLICANT: JORDAO DE MEGALHAES, GUILHERME

; APPLICANT: KOCABAS, ARIF

; APPLICANT: CROSBY, JAVIER A.

; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH

; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN

; TITLE OF INVENTION: VIABILITY

; FILE REFERENCE: 539420S

; CURRENT APPLICATION NUMBER: US/11/091,883

; CURRENT FILING DATE: 2005-03-29

; PRIOR APPLICATION NUMBER: 60/556,875

; PRIOR FILING DATE: 2004-03-29

; NUMBER OF SEQ ID NOS: 513

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 114

; LENGTH: 2876

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-091-883-114

Query Match 100.0%; Score 556; DB 12; Length 2876;
Best Local Similarity 100.0%; Pred. No. 8.6e-150;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAAACAAAGATGAGATCAGACACACAGACCGCATCTTCGTC 60
| | | | |
Db 382 AAGGAGCTCATGGGCGCATGGAAACAAAGATGAGATCAGACACACAGACCGCATCTTCGTC 441
| | | | |
QY 61 CAGCGGATCTAGCTGTGTCCAGGCTTCATGCCCTTCTTCCAGGCTGTTCGGAGC 120
| | | | |
Db 442 CAGCGGATCTAGCTGTGTCCAGGCTTCATGCCCTTCTTCCAGGCTGTTCGGAGC 501
| | | | |
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCAATGACTGG 180
| | | | |
Db 502 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCAATGACTGG 561
| | | | |
QY 181 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCCAG 240
| | | | |
Db 562 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGTGGGAAAGGAGCCGTGGACCCAG 621
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QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAGACTCCCTTC 300
| | | | |
Db 622 CTGACACGGCTGGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAGACTCCCTTC 681
| | | | |
QY 301 CCGGACTCAGACACCACCGCGCTCTTCCAAATCAGCGGAGCACTGTCTCTGTG 360
| | | | |
Db 682 CCGGACTCAGACACCACCGCGCTCTTCCAAATCAGCGGAGCACTGTCTCTGTG 741
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Qy	361	CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTGTACCAACGCCCGATGGCCAT	420
Db	742	CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTGTACCAACGCCCGATGGCCAT	801
Qy	421	TACTACGCATCCTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTTCATTGCTGCC	480
Db	802	TACTACGCATCCTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTTCATTGCTGCC	861
Qy	481	CTTATGAAAAAGAGGTGCCTCTCTGCCCCTACCAACAATTTCTAGTGGCCAGCTCATC	540
Db	862	CCTTATGAAAAAGAGGTGCCTCTCTGCCCCTACCAACAATTTCTAGTGGCCAGCTCATC	921
Qy	541	AGCCACTGGAAGGCA	556
Db	922	AGCCACTGGAAGGCA	937

RESULT 4

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US-10-775-169-229
; Sequence 229, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 229
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-229

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Query Match	100.0%;	Score 556;	DB 8;	Length 2937;
Best Local Similarity	100.0%;	Pred. No. 8.7e-150;		
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGGAGCTCATGGGCCATGGAA	CAAGGATGAGATCAGACCA	CAGACGCGGATCTTCGTC 60
DB	250	AAGGAGCTCATGGGCCATGGAA	CAAGGATGAGATCAGACCA	CAGACGCGGATCTTCGTC 309
QY	61	CAGCGGATCTGAAGCTGTGTC	AGGGGTTTCATGCCCCACTT	TTTCAGGCTGTTCGCGAGC 120
DB	310	CAGCGGATCTGAAGCTGTGTC	AGGGGTTTCATGCCCCACTT	TTTCAGGCTGTTCGCGAGC 369
QY	121	ACGGTCAAGCAAGTGGACTTTT	CAGAGGTCGAGAGCCGAGATT	TCATCATCAATGACTGG 180
DB	370	ACGGTCAAGCAAGTGGACTTTT	CAGAGGTCGAGAGCCGAGATT	TCATCATCAATGACTGG 429
QY	181	GTGAAGACACACAAAAGTATGAT	CAGCAACTTGTTCGGAAAGAGCG	CGTGGACCAAG 240
DB	430	GTGAAGACACACAAAAGTATGAT	CAGCAACTTGTTCGGAAAGAGCG	CGTGGACCAAG 489
QY	241	CTCACACGGCTGTGTGTGTAAT	GGCCCTCTACTTCAACGCCAGT	CGGAGACTCCCTTC 300
DB	490	CTCACACGGCTGTGTGTGTAAT	GGCCCTCTACTTCAACGCCAGT	CGGAGACTCCCTTC 549
QY	301	CCGACTCCAGCACCCACCGCCG	CTTTCACAAATCAGACGCGCACT	GTCTCTGTG 360
DB	550	CCGACTCCAGCACCCACCGCCG	CTTTCACAAATCAGACGCGCACT	GTCTCTGTG 609
QY	361	CCCATCATGCTCAGACCCACAGT	TTCAACTATCTAGGTTCCACCGC	CGGATGGCCAT 420
DB	610	CCCATCATGCTCAGACCCACAGT	TTCAACTATCTAGGTTCCACCGC	CGGATGGCCAT 669
QY	421	TACTACGACATCCTGGAACTGCC	CTTACCGGGGACACCCCTCAGCA	TGTTCAATGTGTC 480

Db	670	TACTACGACATCTGGAACTGCCCTACACCGGGACACCCCTCAGCATGTTCTATTGCTGCC	729
Qy	481	CCTTATGAAAAAGAGTGGCCCTCTCTGCCCCACCAACATTTCTGAGTGCCAGCTCATC	540
Db	730	CCTTATGAAAAAGAGTGGCCCTCTCTGCCCCACCAACATTTCTGAGTGCCAGCTCATC	789
Qy	541	AGCCACTGGAAAGGCA	556
Db	790	AGCCACTGGAAAGGCA	805

RESULT 5

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US-11-091-883-113
; Sequence 113, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; TITLE OF INVENTION: VIABILITY
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091.883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 113
; LENGTH: 3273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (23)..(25)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (28)..(28)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (36)..(36)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (38)..(38)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (40)..(40)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1486)..(1486)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1546)..(1546)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1719)..(1719)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1835)..(1835)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:

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NAME/KEY: modified_base
LOCATION: (2081)..(2081)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (2221)..(2224)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (2226)..(2241)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (2300)..(2300)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (2323)..(2323)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (2352)..(2352)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (2442)..(2442)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3174)..(3174)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3177)..(3177)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3179)..(3182)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3184)..(3185)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3187)..(3187)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3189)..(3190)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3195)..(3195)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3200)..(3200)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3202)..(3204)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3206)..(3206)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3218)..(3218)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base

LOCATION: (3221)..(3221)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3240)..(3240)
OTHER INFORMATION: a, c, g, or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (3243)..(3243)
OTHER INFORMATION: a, c, g, or t
US-11-091-883-113

Query Match 100.0%; Score 556; DB 12; Length 3273;

Best Local Similarity 100.0%; Pred. No. 8.9e-150;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 60
DB 454 AAGGAGCTCATGGGCCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 513
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
DB 514 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 573
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCAATCACTGG 180
DB 574 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCAATCACTGG 633
QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 240
DB 634 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCG 693
QY 241 CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
DB 694 CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 753
QY 301 CCCGACTCCAGCACCCACCGCGCCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 360
DB 754 CCCGACTCCAGCACCCACCGCGCCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 813
QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTGAGTTTCAACGCCCGATGGCCAT 420
DB 814 CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTGAGTTTCAACGCCCGATGGCCAT 873
QY 421 TACTACGACATCTCGAATCGCCCTTACCGGGGACACCTTCAGCATGTTTCATTCGTCGC 480
DB 874 TACTACGACATCTCGAATCGCCCTTACCGGGGACACCTTCAGCATGTTTCATTCGTCGC 933
QY 481 CCTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACATTCTGAGTCCCGAGCTCATC 540
DB 934 CCTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACATTCTGAGTCCCGAGCTCATC 993
QY 541 AGCCACTGGAAAGGCA 556
DB 994 AGCCACTGGAAAGGCA 1009

RESULT 6
US-11-094-519A-10
Sequence 10, Application US/11094519A
Publication No. US20050281810A1
GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Jeanne
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0140P
CURRENT APPLICATION NUMBER: US/11/094,519A
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: IL 132558
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 2438
TYPE: DNA
ORGANISM: Homo sapiens
US-11-094-519A-10

Query Match
Best Local Similarity 86.2%; Score 479; DB 12; Length 2438;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAGGAGCTCATGGGGCCATGAAACAAAGGTATGATCAGACACACAGCGGATCTTCGTC 60
454 AAGGAGCTCATGGGGCCATGAAACAAAGGTATGATCAGACACACAGCGGATCTTCGTC 513
61 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 120/
514 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 573
121 ACGTCAAGCAAGTGCATCTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 180
574 ACGTCAAGCAAGTGCATCTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 633
181 GTGAAGACACACAAAGGTATGATCAGCAACTGCTTGGGAAAGAGCCGTTGGACACAG 240
634 GTGAAGACACACAAAGGTATGATCAGCAACTGCTTGGGAAAGAGCCGTTGGACACAG 693
241 CTGACACGGTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 300
694 CTGACACGGTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 753
301 CCGGACTCAGCAGCACCACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 360
754 CCGGACTCAGCAGCACCACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 813
361 CCGGACTCAGCAGCACCACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 420
814 CCGGACTCAGCAGCACCACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 873
421 TACTACGATCTGGAAGTGCCTTCCACCGGGGACACCTCAGCATGTTTCATTTGCTGC 479
874 TACTACGATCTGGAAGTGCCTTCCACCGGGGACACCTCAGCATGTTTCATTTGCTGC 932

RESULT 7
US-11-136-527-3753
Sequence 3753, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3753
LENGTH: 3053
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-3753

Query Match
Best Local Similarity 75.8%; Score 421.6; DB 12; Length 3053;
Matches 472; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

1 AAGGAGCTCATGGGGCCATGAAACAAAGGTATGATCAGACACACAGCGGATCTTCGTC 60
425 AAGGAGCTCATGGGGCCATGAAACAAAGGTATGATCAGACACACAGCGGATCTTCGTC 484

61 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 120
485 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 544
121 ACGTCAAGCAAGTGCATCTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 180
545 ACGTCAAGCAAGTGCATCTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 604
181 GTGAAGACACACAAAGGTATGATCAGCAACTGCTTGGGAAAGAGCCGTTGGACACAG 240
605 GTGAAGACACACAAAGGTATGATCAGCAACTGCTTGGGAAAGAGCCGTTGGACACAG 664
241 CTGACACGGTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 300
665 CTGACACGGTGTGTCAGGGCTTCATGCCCACTTCTCAGGGCTGTTCCGGAGC 724
301 CCGGACTCAGCAGCACCACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 360
725 TTAGAGGCGACACACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 784
361 CCGGACTCAGCAGCACCACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 420
785 CCGGACTCAGCAGCACCACCGCGCTCTTCCAAATCAGAGCGGAGCAGTGTCTCTGTG 844
421 TACTACGATCTGGAAGTGCCTTCCACCGGGGACACCTCAGCATGTTTCATTTGCTGC 480
845 GAGTACGATCTGGAAGTGCCTTCCACCGGGGACACCTCAGCATGTTTCATTTGCTGC 904
481 CCGTATGAAGAGAGTGCCTTCTCTGCCCTCACCACCATCTGAGTCCCGAGCTCAGC 540
905 CCGTATGAAGAGAGTGCCTTCTCTGCCCTCACCACCATCTGAGTCCCGAGCTCAGC 964
541 AGCCACTGGAAAGGCA 556
965 AGCAATGGAAGCA 980

RESULT 8
US-10-750-185-46781
Sequence 46781, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: Denise, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46781
LENGTH: 1404
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-46781

Query Match
Best Local Similarity 30.0%; Score 166.8; DB 8; Length 1404;
Matches 186; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

194 CAAAGGATGATCAGCAACTTGTCTTGGGAAAGAGCCGTTGGACAGCTGACACCGCTGG 253
958 CCAATAGGATGATCAGCAACTTGTCTTGGGAAAGAGCCGTTGGACAGCTGACACCGCTGG 1017
254 TGTCTGATGCTCTTCTTCTTCAACCGGAGTGAAGACTCCCTTCCCGAGCTCAGCA 313

Qy	287	GGAGACTCCCTTCCCGACTCCAGCACCCACCGCGCGCTCTTCACAAATCAGACGGCA	346
Db	578	GGAAATCATCGGTTTCAACCCGAGACACAAAGAAACGCATTTTCGTGGCAGCCGACCGGA	637
Qy	347	GCACGTGCTCTGTGGCCATGATGGCTCAGACCAACAAAGTTCAAATCTATCTGAGTTCACCA	406
Db	638	AATCCTATCAAGTGCCATGCTGGCCAGCTCTCCGTGTTCCGGTGGCGACAAGTG	697
Qy	407	CGCCGATGGCCATTATACGACATCTTGGAACTGCCCTTACCACGGGACACCCCTCAGCA	466
Db	698	CCCCCAATGATTATATGGTACAACTTTCATTGAATGCCCTTACCACGGGGAAAGCATCAGCA	757
Qy	467	TGTTTCATTGTCGCCCTTATGAAAAGAGGTGCCTCTCTGCGCTCCACCAACATTCGA	526
Db	758	TGCTGATTGGACTGCGACTGAGAGCTCCATCCGCTGTCTGCGCATCCACACATCA	817
Qy	527	GTGCCCGACTCATCAGCCACTGGAAAGGCA	556
Db	818	GCACCAAGACCATAGACAGCTGGATGAGCA	847

```

RESULT 12
US-10-821-234-636
; Sequence 636, Application US/10821234
; Publication No. U320050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 636_
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-636

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Query Match	20.5%	Score 114;	DB 8;	Length 1197;
Best Local Similarity	54.9%	Pred. No. 7.9e-23;		
Matches 247; Conservative	0;	Mismatches 200;	Indels 3;	Gaps 1.

110	QY	TGTTCCGGACGCGTCAAGAAAGTGACTTTTCAGAGGTGGAGAGCCAGATTCATCA	169
398	Db	TGTTCCAGTGTGAGGTCGGAAATGTGAATTTTGAGGATCCAGCCTCTGCCTGTGATTCCA	457
170	QY	TCAATGACTGGGTGACACACACACAAAAGGTATGATCAGCAATTCCTTGGGNAAGGAG	229
458	Db	TCAATGCATGGGTTAAAAATGAAACCAAGGATATGATTGACATCTGCTGCCCAGATC	517
230	QY	CCGTGGA---CAGCTGACACGGCTGCTGTGGTGAATGCCTCTACTTCAACGGCCAGT	286
518	Db	TTATTGATGTGTGCTCACCAGACTGCTCTCGTCAACGAGTGTATTTCAAGGCTCTGT	577
287	QY	GGAAGACTCCCTTCCCGACTCCAGCACCCACCGCGCCTCTTCCACAAATCAGACGGCA	346
578	Db	GGAAATCAGGGTTCCAAACCCGAGAACACAAAGAAACGCATTTTCGTGGCAGCCGCGGA	637
347	QY	GCATCTCTCTGTGCCCATGATGGCTCAGACCAACAAAGTTCAACTATATCTGAGTTCACCA	406
638	Db	AATCTTATCAAGTGCCAATGCTGGGCCAGCTCTCCGTGTTCCGGTGTGGGTTCGCAAGTG	697
407	QY	CGCCCGATGCCATTACTACGACATCTCGAACTCGCCTACCAACGGGGACACCTTCAGCA	466
698	Db	CCCCCAATGATTATTGGTACCACTTCATTGAATCGCCCTACCAACGGGGAAAGCATCAGCA	757
467	QY	TGTTCAATTCGTCCCTTTATGAAAAAGAGGTGCTCTCTCTGCGCCTCACCAACATTCGA	526

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Db      758  TGTGATTGCACCTCCGACTGAGAGCTCCACTCCGCTGCTGTGCCATCATCCACACATCA 817
Qy      527  GTGCCAGCTCATCAGCCATCGGAAGGCA 556
Db      818  GCACCAAGACCATAGACAGCTGGATGAGCA 847

RESULT 13
US-11-186-284-184
; Sequence 184, Application US/11186284
; Publication No US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2ENM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 2129
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210) ... (1406)
US-11-186-284-184

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Query Match	20.5%;	Score 114;	DB 12;	Length 2129;
Best Local Similarity	54.9%;	Pred. No. 9.3e-23;		
Matches .247;	Conservative 0;	Mismatches 200;	Indels 3;	Gaps 1;
QY	110	TGTTCCGGAGCAGGTCACAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTCA	TC	169
Db	607	TTGTTCCAGTGTGAGGTCGCGAATGTGAACTTTGAGGATCCAGCCTCTGCCTGTGATTCCA		666
QY	170	TCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAG		229
Db	667	TCAATGCAATGGGTTAAAAATGAACACGAGGATATGATTGACATCTGCTGTCCCAGATC		726
QY	230	CCGTGGA---CCAGCTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGT		286
Db	727	TTATTGATGGTGTGCTCACAGACTGGTCTCTCGTCAACGCAGTGTATTTCAAGGGTCTGT		786
QY	287	GGAAGACTCCCTTCCCGACTCCAGCACCCACCGCGCCTCTTCCACAAATCAGACGGCA		346
Db	787	GGAATACAGGTTCCACCCGAGAACACAAAGAACGCACATTTCTGGTGGCAGCCGACGGGA		846
QY	347	GCACGTGCTCTGTGCCCATGATGGCTCAGACCAACAAAGTTTCAACTATATCTGAGTTCACCA		406
Db	847	AATCCTATCAAGTGCATGCTGGCCACGCTCTCCGTGTTCCGGTGTGGGTGCACAGTG		906
QY	407	CGCCGATGGCCATTACTAGCAATCCTGGAACTGCCCTTACACGGGGACACCCCTCAGCA		466
Db	907	CCCCCAATGATTATGGTACAACTTCATTGAACTGCCCTTACACGGGGAAAGCATCAGCA		966

QY 467 TGTTCATTCCTGCCCTTATGAAAGAGGTGCTCTCTCTGCTCCCTCACCAACATTCTGA 526
Db 967 TGTGATTGCACTGCCGAGCTGAGAGCTCCACTCGCTGTCTGCCATCATCCACACATCA 1026
QY 527 GTGCCAGCTCATCAGCCACTGGAAAGCA 556
Db 1027 GCACCAAGACCATAGACAGCTGGATGAGCA 1056

RESULT 14
US-11-245-147-20
; Sequence 20, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-245-147-20

Query Match 17.7%; Score 98.4; DB 9; Length 1212;
Best Local Similarity 52.9%; Pred. No. 2.4e-18;
Matches 235; Conservative 0; Mismatches 206; Indels 3; Gaps 1;
QY 110 TGTTCGGAGCAGCGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCA 169
Db 409 TGTTCAGTGTGAAGTGCAGATGTGAATTCAGGACCCAGCTCTGCTCTGAGTCCA 468
QY 170 TCAATGACTGGGTGAAGACACACAAAAAGGTATGATCAGCAACTTTGCTT---GGGAAAG 226
Db 469 TCAATTTTGGGTCAAAAATGAGACCAGGGGCATGATTGATAACCTGCTTTCCCAAAATC 528
QY 227 GAGCCGTGACACAGCTGACAGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGT 286
Db 529 TGATCGATGTGCGCTTACAGGCTGGTCTCTGTTAATGCAAGTGTATTTCAGGGGTTTGT 588
QY 287 GGAAGACTCCCTTCCCGACTCCAGACCCACCGCGCTCTTCCCAAAATCAGACGGCA 346
Db 589 GGAAGTCTCGTTTCAACAGAGACACAAAGAACCGGACATTCGTGGCAGGTGATGGGA 648
QY 347 GCACTGTCTGTGCGCCATGATGGCTCAGACCAACAAAGTTTCAACTATATGAGTTTCA 406
Db 649 AATCCTACCAAGTACCATGTTGGCTCAGCTCTCTGTGTTCCGCTCAGGGTCTACCA 708
QY 407 CGCCCGATGCCATTACTAGCAATCCTGGAACTGCCCTACCAAGGGGACACCTTCAGCA 466
Db 709 CCCCGAATGGCTTATGGTACAACTTCAATTGAGTGGCTTACCATGTTGAGAGCATCAG 768
QY 467 TGTTCATTCGCTCCCTTATGAAAAGAGGTGCTCTCTCTGCTCCCTCACCAACATTCTGA 526
Db 769 TGTGATCGCCCTGCGCAACAGAGGTCCACCCCACTGTCTGCCATCATCCCTCATCA 828
QY 527 GTGCCAGCTCATCAGCCACTGGA 550

Db 829 CTACCAAGACCATTCATGACTGGA 852
RESULT 15
US-11-136-527-1947
; Sequence 1947, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AWI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1947
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1947

Query Match 17.0%; Score 94.6; DB 12; Length 1963;
Best Local Similarity 49.3%; Pred. No. 3.4e-17;
Matches 263; Conservative 4; Mismatches 263; Indels 3; Gaps 1;
QY 21 GAACAAGGATGATGATCAGACACAGACGGGATCTTCGTCAGCGGGATCTGAAGCTGT 80
Db 309 GAATAAAGACATWTGACCGTGGCCAATGCTGTGTTGTGTCAGGAATGGCTTTAAAGTGA 368
QY 81 CCAGGGCTTCATGCCCCCACTCTTCAGGCTGTTCGGGAGACGGTCAAGAGTGGACTT 140
Db 369 AGTGCTTTTGACGAAGAAACAAAGAGGTGTTTCAGTGTGAAGTACAGAGTGTGAATT 428
QY 141 TTCAGAGGTGGAGAGAGCCAGATTTCATCAATGATCTGGTGAAGACACACAAAAAG 200
Db 429 CCAGGACCCGGCTCTGCTTGTGATGCCATCAATTTTGGGTCAAAAATGAGACGGGG 488
QY 201 TATGATCAGCAACTTGTCTT---GGGAAAGGAGCCGCTGGACAGCTGACAGGCTGTGCT 257
Db 489 CATGATTGACAACTTACTTTCCCNMAAAMWRAWRATAGTGTCTTTACCAAACTGGTCT 548
QY 258 GGTGAATGCCCTTACTTCAACGGCCAGTGGAAAGACTCCCTTCCCGACTCCAGCACCA 317
Db 549 CGTTAACCGAGTGTATTTCAAGGGTTTGTGGAATCCCGGTTTCAACCTGAGAACACGA 608
QY 318 CCGCCGCTCTTCCCAAAATCAGACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGAC 377
Db 609 GAAACGGACCTTCGTGGCAGGTGATGGAAATCTCTACCAAGTACCATGCTAGCCAGCT 668
QY 378 CAACAAGTTTCAATATATGAGTTTCAACGCGCCGATGSCCAATTAATAGCAATCTGGA 437
Db 669 CTCCTGTTCGCTCTGCGTCTACCAAAACCCCAATGGCTTATGTTACAACTTCAATGA 728
QY 438 ACTGCCCTTACCAAGGGGACACCTCAGCATGTTTCAATGCTGCCCTTATGAAAAGAGGT 497
Db 729 GTACCTCTACCATGTTGAGAGCATCAGCATGTTGATCGCCCTGCGCAACAGAGAGTCCAC 788
QY 498 GCTCTCTCTGCGCTCACCAACATTTCTGAGTGGCCAGCTCATCAGCCACTGGA 550
Db 789 CCACTGTGCGCCATCATCCCTCACATCAGTACCAAGACCATCAATAGTGA 841

Search completed: March 10, 2006, 01:54:22
Job time : 322 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:05 ; Search time 5640 Seconds
(without alignments)
4612.344 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793
Perfect score: 556
Sequence: 1 aaggagctcatggggccatg.....catcagccactgaaaggca 556

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	659	CN309034	CN309034 170004247
2	556	100.0	813	2 BG829624	BG829624 602763976
3	556	100.0	932	2 BE905905	BE905905 601495570
4	556	100.0	1027	5 BX396693	BX396693 BX396693
5	556	100.0	1168	10 AY402982	AY402982 Pan trogl
6	556	100.0	1209	10 AY402981	AY402981 Homo sapi
7	556	100.0	1474	4 CR614829	CR614829 full-lenq
8	555.6	100.0	1019	5 BX379573	BX379573 BX379573
9	555.6	100.0	1085	5 BX335507	BX335507 BX335507
10	555.2	100.0	1028	5 BX425037	BX425037 BX425037
11	554.4	99.7	1116	5 BX446279	BX446279 BX446279
12	550.8	99.1	817	3 BI870529	BI870529 603394394
13	550.2	99.0	894	6 CA489543	CA489543 AGENCOURT
14	549.2	98.8	1029	5 BX382561	BX382561 BX382561
15	545	98.0	749	2 BI224436	BI224436 602940982
16	545	98.0	823	6 CD609138	CD609138 560817410
17	545	98.0	1124	5 BX378424	BX378424 BX378424
18	544.6	97.9	832	5 BX379609	BX379609 BX379609
19	544.4	97.9	996	5 BX377975	BX377975 BX377975
20	544	97.8	616	7 CN485218	CN485218 BX24605.Y
21	543.6	97.8	1093	5 BX356157	BX356157 BX356157
22	543.4	97.7	694	1 AUI139624	AUI139624 AUI139624

23	543.4	97.7	975	1	AL545394	AL545394
24	542	97.5	971	5	BX417006	BX417006
25	541.8	97.4	931	5	BU540881	BU540881 AGENCOURT
26	541.8	97.4	1010	5	BX340248	BX340248 BX340248
27	541.6	97.4	1017	5	BX439383	BX439383 BX439383
28	540.6	97.2	853	5	BX344504	BX344504 BX344504
29	539	96.9	581	3	BP237212	BP237212 BP237212
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32	532.8	95.8	1019	1	AL550303	AL550303 AL550303
33	532	95.7	968	5	BX355763	BX355763 BX355763
34	531.6	95.6	1107	5	BX424917	BX424917 BX424917
35	530	95.3	681	6	CF132569	CF132569 UI-HF-PQO
36	529	95.1	960	5	BX335314	BX335314 BX335314
37	526.6	94.7	948	5	BX381412	BX381412 BX381412
38	520.4	93.6	899	6	CD609140	CD609140 56081757J
39	519	93.3	588	3	BM127625	BM127625 ie97f09.Y
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41	517	93.0	869	3	BQ218607	BQ218607 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS CN309034 659 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424711627 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN309034
VERSION CN309034.1 GI:47325448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
AUTHORS Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.7e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCCCCTACCAACATTTCTGAGTGCCCGAGCTCAT 540
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QY 541 AGCCACTGGAAGGCA 556
Db 598 AGCCACTGGAAGGCA 613

RESULT 2
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LOCUS 602763976F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899139 5',
DEFINITION mRNA sequence.
ACCESSION BG829624
VERSION BG829624.1 GI:14177211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
Cloning Strategy: In-cyte Genomics, Inc.
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Place: LNCMI790 row: h column: 20
High quality sequence stop: 810.
Location/Qualifiers
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/organism="Homo sapiens"
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/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 210 CAGCGGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 269
QY 121 ACGGTCACAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTATCATCAATGACTGG 180
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Db 450 CCGGACTCCAGCACCAACCGCGCCCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 509
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTCACACGCCCGATGGCCAT 420
Db 510 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTCACACGCCCGATGGCCAT 569
QY 421 TACTACGACATCCTGGAATCGCCCTACACGGGGACACCCCTCAGCATGTTCAATGTC 480
Db 570 TACTACGACATCCTGGAATCGCCCTACACGGGGACACCCCTCAGCATGTTCAATGTC 629
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCCCCTACCAACATTTCTGAGTGCCCGAGCTCAT 540
Db 630 CTTTATGAAAAGAGTGCTCTCTCTGCCCCTACCAACATTTCTGAGTGCCCGAGCTCAT 689
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Db 690 AGCCACTGGAAGGCA 705

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LOCUS 601495570F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897737 5',
DEFINITION mRNA sequence.
ACCESSION BG829624
VERSION BG829624.1 GI:10399246
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
Hominidae; Homo.					
REFERENCE	1	(bases 1 to 932)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM9692 row: k column: 18 High quality sequence stop: 672.				
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	Best Local Similarity	100.0%; Pred. No. 5.2e-141;			
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QY	301	CCCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCATGTCTCTGTG 360			
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QY	361	CCCATGATGCTCAGACCAACAAGTTTCAACTATACTGAGTTTCACACGCCCGATGCCAT 420			
Db	429	CCCATGATGCTCAGACCAACAAGTTTCAACTATACTGAGTTTCACACGCCCGATGCCAT 488			
QY	421	TACTAAGCATCTGGAACTGCCCTACACGGGGACACCTTCAGACATGTTTCATGTGCC 480			
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Qy	361	CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTGTTCACACGCCGATGGCCAT	420
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Qy	481	CTTTATGAAAAGAGGTGCCTCTCTCTGCGCCTTCACCAACATTCCTGAGTGCCAGCTCATC	540
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Db	974	AGCCACTGGAAAGGCA	989
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DEFINITION	Pan troglodytes SERPINE1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		GSS 15-DEC-2003
ACCESSION	AY402982		
VERSION	AY402982.1	GI:39758965	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.		
AUTHORS	1 (bases 1 to 1168) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1168)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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Best Local Similarity	100.0%;	Pred. No. 5.6e-141;	
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Qy	61	CAGCGGATCTGAAGCTGGTCCAGGGCTTATGCCCCCACTTCTTCAAGCTTTCCGAGC	120
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Qy	121	ACGGTCAAGCAAGTGGA	CTTTTCAGAGGTTGGAGAGCCAGATTTCATCATCAATGACTGG	180
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Qy	241	CTGACACGGCTGGTGTG	TGGTGAATGCCCTCTTACTTTCAACGCCAGTGGAGACTCCCTTC	300
Db	547	CTGACACGGCTGGTGTG	TGGTGAATGCCCTCTTACTTTCAACGCCAGTGGAGACTCCCTTC	606
Qy	301	CCGAGCTCAGACACCA	CCGCGGCTCTTTCACAATCAGACGCGAGCACTGTCTCTGTG	360
Db	607	CCGAGCTCAGACACCA	CCGCGGCTCTTTCACAATCAGACGCGAGCACTGTCTCTGTG	666
Qy	361	CCCATGATGCTCAGACCA	CAAGTTCAACTATACTGAGTTTCAACACGCCGATGGCCAT	420
Db	667	CCCATGATGCTCAGACCA	CAAGTTCAACTATACTGAGTTTCAACACGCCGATGGCCAT	726
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Qy	481	CTTTATGAAAAAGAGGTG	CCCTCTCTCTGCGCTTACCAACAATCTTGAGTCCGACGCTCATC	540
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Db	847	AGCCACTGGAAAGGCA	862	
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DEFINITION	Homo sapiens SERPINE1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.			
ACCESSION	AY402981			
VERSION	AY402981.1	GI:39758964		
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 1209) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science	302 (5652), 1960-1963 (2003)		
PUBMED	14671302			
REFERENCE	2 (bases 1 to 1209) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission			
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
JOURNAL	This sequence was made by sequencing genomic exons and ordering them based on alignment.			
COMMENT	Location/Qualifiers			
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	/gene="SERPINE1"			

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Hominidae; Homo.
1 (bases 1 to 1019)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30450782.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI035CF07QPI&c=4412.f.

FEATURES
source

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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 100.0%; Score 556; DB 5; Length 1019;
Best Local Similarity 99.8%; Pred. No. 6.9e-141;
Matches 555; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAAGAGTATGATCAGCACACAGAGCGGATCTTCGTC 60
DB 432 AAGGAGCTCATGGGGCCATGGAAAGAGTATGATCAGCACACAGAGCGGATCTTCGTC 491
QY 61 CAGCGGATCTCAAGCTGTGTGAGGCTTCATGCCCTCTTTCAGGCTGTTCGGAGC 120
DB 492 CAGCGGATCTCAAGCTGTGTGAGGCTTCATGCCCTCTTTCAGGCTGTTCGGAGC 551
QY 121 ACGGTCAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCACTGG 180
DB 552 ACGGTCAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCACTGG 611
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGAGCGGTGGACCA 240
DB 612 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGAGCGGTGGACCA 671
QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
DB 672 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 731
QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCCAATCAGAGCGGAGCACTGTCTCTGTG 360
DB 732 CCGGACTCCAGCACCCACCGCGCTCTTCCCAATCAGAGCGGAGCACTGTCTCTGTG 791
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCATCTAGATTCACCAACCGCGGATGGCCAT 420
DB 792 CCCATGATGGCTCAGACCAACAAAGTTCATCTAGATTCACCAACCGCGGATGGCCAT 851
QY 421 TACTACGATCCTGGACTGGCTCCCTACACGGGGACCCCTCAGCATGTTCTGTCGCC 480
DB 852 TACTACGATCCTGGACTGGCTCCCTACACGGGGACCCCTCAGCATGTTCTGTCGCC 911
QY 481 CCTTATGAAAAGAGGTGCTCTCTCTGCGCTCAGCAATCTCTGAGTGGCCAGCTCATC 540
DB 912 CCTTATGAAAAGAGGTGCTCTCTCTGCGCTCAGCAATCTCTGAGTGGCCAGCTCATC 971
QY 541 AGCCACTGGAAGAGCA 556

Db 972 AGCCACTGGAAGAGCA 987

RESULT 9
BX335507

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BX335507 1085 bp mRNA linear EST 07-APR-2004
clone CS0DI015YB08 5-PRIME, mRNA sequence.
BX335507
BX335507.2 GI:46266450
EST
Homo sapiens (human)
Homo sapiens
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1085)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30312419.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI015DA04QPI&c=4412.f.

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI015YB08"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 100.0%; Score 556; DB 5; Length 1085;
Best Local Similarity 99.8%; Pred. No. 7e-141;
Matches 555; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAAGAGTATGATCAGCACACAGAGCGGATCTTCGTC 60
DB 421 AAGGAGCTCATGGGGCCATGGAAAGAGTATGATCAGCACACAGAGCGGATCTTCGTC 480
QY 61 CAGCGGATCTCAAGCTGTGTGAGGCTTCATGCCCTCTTTCAGGCTGTTCGGAGC 120
DB 481 CAGCGGATCTCAAGCTGTGTGAGGCTTCATGCCCTCTTTCAGGCTGTTCGGAGC 540
QY 121 ACGGTCAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCACTGG 180
DB 541 ACGGTCAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATCACTGG 600
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGAGCGGTGGACCA 240
DB 601 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGAGCGGTGGACCA 660
QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
DB 661 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 720
QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCCAATCAGAGCGGAGCACTGTCTCTGTG 360

Qy 1 AAGGAGCTCATGGGGCCATGGAACTAGGATGAGATCAGCACACAGACGGATCTTCGTC 60

Db 438 AAGGAGCTCATGGGGCCATGGAACTAGGATGAGATCAGCACACAGACGGATCTTCGTC 497

This sequence belongs to sequence cluster 4412.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=XCLOBA0012E03BP1&c=4412.f>.

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Location/Qualifiers
1..1116
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="XCL082001ZE03"
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/clone_lib="Homo sapiens PLACENTA"
/Note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match          99.7%; Score 554.4; DB 5; Length 1116;
Best Local Similarity 99.3%; Pred. No. 1.5e-140;
Matches 552; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGATGATCAGCACACAGACGCGATCTTCGTC 60
Db 258 AAGGAGCTCATGGGGCCATGGAAACAGGATGATGATCAGCACACAGACGCGATCTTCGTC 317
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
Db 318 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 377
QY 121 ACGGTCAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTTCATCAATCAATGACTGG 180
Db 378 ACGGTCAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 437
QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCA 240
Db 438 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCA 497
QY 241 CTGACACGGCTGTGTGTGTAATGCCCTCTACTTTCAGCGGCAGTGAAGACTCCCTTC 300
Db 498 CTGACACGGCTGTGTGTGTAATGCCCTCTACTTTCAGCGGCAGTGAAGACTCCCTTC 557
QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGAGCGGAGCACTGTCTCTGTG 360
Db 558 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGAGCGGAGCACTGTCTCTGTG 617
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCACTATCTAGATTTCACACCGCGGATGCCCAT 420
Db 618 CCCATGATGGCTCAGACCAACAAAGTTCACTATCTAGATTTCACACCGCGGATGCCCAT 677
QY 421 TACTAGACATCTCTGGAATCGCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 480
Db 678 TACTAGACATCTCTGGAATCGCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 737
QY 481 CCTTATGAAAAGAGTGCTCTCTCTGCCCTCACCACATTTCTCAGTGGCCAGCTCATC 540
Db 738 CCTTATGAAAAGAGTGCTCTCTCTGCCCTCACCACATTTCTCAGTGGCCAGCTCATC 797
QY 541 AGCCACTGGAAAGGCA 556
Db 798 AGCCACTGGAAAGGCA 813

RESULT 12
BI870529
LOCUS 603394394F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5404558 5',
DEFINITION mRNA sequence.
ACCESSION BI870529
VERSION BI870529.1 GI:16044202
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 817)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
```

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Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12031 row: k column: 23
High quality sequence stop: 814.

FEATURES
Location/Qualifiers
source
1..817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5404558"
/tissue_type="adenocarcinoma, cell_line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/Note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match          99.1%; Score 550.8; DB 3; Length 817;
Best Local Similarity 99.6%; Pred. No. 1.3e-139;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGATGATCAGCACACAGACGCGATCTTCGTC 60
Db 228 AAGGAGCTCATGGGGCCATGGAAACAGGATGATGATCAGCACACAGACGCGATCTTCGTC 287
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
Db 288 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 347
QY 121 ACGGTCAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 180
Db 348 ACGGTCAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTTCATCAATGACTGG 407
QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCA 240
Db 408 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCA 467
QY 241 CTGACACGGCTGTGTGTGTAATGCCCTCTACTTTCAGCGGCAGTGAAGACTCCCTTC 300
Db 468 CTGACACGGCTGTGTGTGTAATGCCCTCTACTTTCAGCGGCAGTGAAGACTCCCTTC 527
QY 301 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGAGCGGAGCACTGTCTCTGTG 360
Db 528 CCGGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGAGCGGAGCACTGTCTCTGTG 587
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCACTATCTAGATTTCACACCGCGGATGCCCAT 420
Db 588 CCCATGATGGCTCAGACCAACAAAGTTCACTATCTAGATTTCACACCGCGGATGCCCAT 647
QY 421 TACTAGACATCTCTGGAATCGCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 480
Db 648 TACTAGACATCTCTGGAATCGCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 707
QY 481 CCTTATGAAAAGAGTGCTCTCTCTGCCCTCACCACATTTCTCAGTGGCCAGCTCATC 540
Db 708 CCTTATGAAAAGAGTGCTCTCTCTGCCCTCACCACATTTCTCAGTGGCCAGCTCATC 767
QY 541 AGCCACTGGAAAGG 554
Db 768 AGCCACTGGAAAG 781

RESULT 13
CA489543
LOCUS CA489543 894 bp mRNA linear EST 14-NOV-2002
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AGENCY: 10810368 MAPcL Homo sapiens cDNA clone IMAGE:6722018 5', mRNA sequence.
CA489543
VERSION CA489543.1 GI:24952334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NTH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14284 row: b column: 02
High quality sequence stop: 674.
Location/Qualifiers
1..894
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/mol_type="mRNA"
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/lab_host="EMDH10B"
/clone_lib="MAPcL"
/notes="Vector: pCMV-SPORT6; Site 1: EcorV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."
ORIGIN
Query Match 99.0%; Score 550.2; DB 6; Length 894;
Best Local Similarity 99.5%; Pred. No. 2e-139;
Matches 552; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGGAAACAGGATGAGATCAGCACACAGCCGATCTTCGTC 60
DB 298 AAGGAGCTCATGGGCGCATGGAAACAGGATGAGATCAGCACACAGCCGATCTTCGTC 357
QY 61 CAGCGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCCGGAGC 120
DB 358 CAGCGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCCGGAGC 417
QY 121 ACGGTCAAGCAAGTGAATCTTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 180
DB 418 ACGGTCAAGCAAGTGAATCTTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGACTGG 477
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGAGCCGTGGACCAAG 240
DB 478 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGAGCCGTGGACCAAG 537
QY 241 CTGACAGGCTGGTGTGATGTCCTTCTACTTCAACGGCGAGTGGAAAGATCTCCCTTC 300
DB 538 CTGACAGGCTGGTGTGATGTCCTTCTACTTCAACGGCGAGTGGAAAGATCTCCCTTC 597
QY 301 CCGGACTCCAGACACCAACCGCGCTCTTCCCAATCAGAGCGGAGCTGCTCTGTG 360
DB 598 CCGGACTCCAGACACCAACCGCGCTCTTCCCAATCAGAGCGGAGCTGCTCTGTG 657

QY 361 CCATGATGCTCAGACCAACAGTTCACTACTACTGAGTTCCACGCGCGATGCCAT 420
DB 658 CCATGATGCTCAGACCAACAGTTCACTACTACTGAGTTCCACGCGCGATGCCAT 717
QY 421 TACTAGACATCTGGAACCTGCCCTACACGGGGACACCTCAGCATGTTCAATTGCTGCC 480
DB 718 TACTAGACATCTGGAACCTGCCCTACACGGGGACACCTCAGCATGTTCAATTGCTGCC 777
QY 481 CTTATGAAAAGAGGTGCTCTCTGCTCCTCACCAATTCAGTGCCTCAGTGCCTCAGTGCCTC 540
DB 778 CTTATGAAAAGAGGTGCTCTCTGCTCCTCACCAATTCAGTGCCTCAGTGCCTCAGTGCCTC 837
QY 541 AGCCCTGGAAGGC 555
DB 838 AGCCCTGGAAGGC 852
RESULT 14
BX382561
LOCUS
DEFINITION 1029 bp mRNA linear EST 28-APR-2004
clone CS0D1082YB17 5-PRIME, mRNA sequence.
ACCESSION BX382561
VERSION BX382561.2 GI:46832678
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1029)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459067.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1082CA09QPI&c=4412.f.
Location/Qualifiers
1..1029
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1082YB17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 98.8%; Score 549.2; DB 5; Length 1029;
Best Local Similarity 98.6%; Pred. No. 3.9e-139;
Matches 548; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGGAAACAGGATGAGATCAGCACACAGCCGATCTTCGTC 60
DB 437 AAGGAGCTCATGGGCGCATGGAAACAGGATGAGATCAGCACACAGCCGATCTTCGTC 496
QY 61 CAGCGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCCGGAGC 120
DB 497 CAGCGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCCGGAGC 556


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QY 121 ACGGTCAAGCAAGTGACCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATCACTGG 180
Db 557 ACGGTCAAGCAAGTGACCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATCACTGG 616
QY 181 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAGAGGAGCCGTGGACCG 240
Db 617 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAGAGGAGCCGTGGACCG 676
QY 241 CTGACACGGCTGGTGTGGTGAATGCGCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
Db 677 CTGACACGGCTGGTGTGGTGAATGCGCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 736
QY 301 CCGGACTCCAGCACCCACACCGCGCTCTTCCCAAATCAGACGGCAGCACTGTCTGTG 360
Db 737 CCGGACTCCAGCACCCACACCGCGCTCTTCCCAAATCAGACGGCAGCACTGTCTGTG 796
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCCGATGGCCAT 420
Db 797 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCCGATGGCCAT 856
QY 421 TACTACGACATCTGGAACTGCGCTTACCACGGGGACACCCCTCAGCATGTTTCAATGCTGCC 480
Db 857 TACTACGACATCTGGAACTGCGCTTACCACGGGGACACCCCTCAGCATGTTTCAATGCTGCC 916
QY 481 CTTTATGAAAAAGAGTGCTCTCTGTGCCCTCACCACAACTTCTGAGTGCCAGCTCATC 540
Db 917 CTTTATGAAAAAGAGTGCTCTCTGTGCCCTCACCACAACTTCTGAGTGCCAGCTCATC 976
QY 541 AGCCACTGGAAGGCA 556
Db 977 AGCCACTGGAAGGCA 992
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RESULT 15
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LOCUS 602940982F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5104076 5',
DEFINITION mRNA sequence.
ACCESSION BI224426
VERSION BI224426.1 GI:14677870
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 749)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11251 row: c column: 21
High quality sequence stop: 744.
FEATURES
Location/Qualifiers
1..749
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5104076"
/tissue_type="cervical"
/lab_host="DH10B"
/clone_lib="NIH MGC 12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
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Technologies."
ORIGIN
Query Match 98.0%; Score 545; DB 2: Length 749;
Best Local Similarity 99.8%; Pred.No.5.1e-138;
Matches 556; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 AAGGAGCTTCATGGGGCCATGGAAACAAGGATGAGATCAGACACACAGACGCGATCTTCGTC 60
Db 14 AAGGAGCTTCATGGGGCCATGGAAACAAGGATGAGATCAGACACACAGACGCGATCTTCGTC 73
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGAGC 120
Db 74 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGAGC 133
QY 121 ACGGTCAAGCAAGTGACCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATCACTGG 180
Db 134 ACGGTCAAGCAAGTGACCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATCACTGG 193
QY 181 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAGAGGAGCCGTGGACCG 240
Db 194 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAGAGGAGCCGTGGACCG 253
QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
Db 254 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 313
QY 301 CCGGACTCCAGCACCCACACCGCGCTCTTCCCAAATCAGACGGCAGCACTGTCTGTG 360
Db 314 CCGGACTCCAGCACCCACACCGCGCTCTTCCCAAATCAGACGGCAGCACTGTCTGTG 373
QY 361 CCCATG-ATGGCTCAGACCAACAAGTTCAAATATCTAGTTTCAACACCGCCGATGGCCA 419
Db 374 CCCATGATGGCTCAGACCAACAAGTTCAAATATCTAGTTTCAACACCGCCGATGGCCA 433
QY 420 TTACTACGACATCTGGAACTGCCCTTACACGGGAGACACCTTCAAGCATGTTTCAATGCTGC 479
Db 434 TTACTACGACATCTGGAACTGCCCTTACACGGGAGACACCTTCAAGCATGTTTCAATGCTGC 493
QY 480 CCCTTATGAAAAAGAGTGCTCTCTGTGCCCTCACCACAACTTCTGAGTGCCAGCTCAT 539
Db 494 CCCTTATGAAAAAGAGTGCTCTCTGTGCCCTCACCACAACTTCTGAGTGCCAGCTCAT 553
QY 540 CAGCCACTGGAAGGCA 556
Db 554 CAGCCACTGGAAGGCA 570
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Search completed: March 10, 2006, 02:39:59
Job time : 5641 secs